

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:54:36 ; Search time 85 Seconds
(without alignments)
1216.890 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGVWLALASLLHVS.....TIGILSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21.:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2546	94.2	502	11 - Q9JHD6	Q9jhd6 mus musculus
2	1816.5	67.2	511	13 Q03481	Q03481 gallus gall
3	1260	46.6	807	5 Q8T7V5	Q8t7v5 drosophila
4	1254.5	46.4	501	5 Q9X214	Q9x214 heliothis v
5	1242	45.9	496	5 Q9X213	Q9x213 heliothis v
6	1221	45.2	494	5 Q8T7S2	Q8t7s2 drosophila
7	1219	45.1	494	5 Q8T7S3	Q8t7s3 drosophila
8	1214	44.9	494	5 Q8T7S1	Q8t7s1 drosophila
9	1204.5	44.6	509	5 Q8T7S0	Q8t7s0 drosophila
10	1202.5	44.5	523	5 Q8T7R9	Q8t7r9 drosophila
11	1093	40.4	554	5 Q62083	Q62083 caenorhabdi
12	998	36.9	461	5 P91197	P91197 caenorhabdi
13	972.5	36.0	523	5 Q46128	Q46128 heliothis v
14	954	35.3	311	5 Q9VW18	Q9vw18 drosophila
15	950.5	35.2	545	5 Q96631	Q96631 heliothis v
16	949.5	35.1	568	5 Q9NFR5	Q9nfr5 drosophila

17	947.5	35.1	536	5 Q8TOY9	Q8toy9 aplysia cal
18	947	35.0	515	5 Q46133	Q46133 locusta mig
19	944	34.9	542	5 Q18556	Q18556 caenorhabdi
20	941.5	34.8	552	5 P91765	P91765 myzus persi
21	938.5	34.7	537	5 Q8U941	Q8u941 myzus persi
22	937.5	34.7	536	5 Q8T9S0	Q8t9s0 aplysia cal
23	933	34.5	512	11 Q91X60	Q91x60 mus musculu
24	925.5	34.2	580	5 Q9VC72	Q9vc72 drosophila
25	921	34.1	629	11 Q9ET51	Q9et51 mus musculu
26	920	34.0	495	11 Q8R493	Q8r493 mus musculu
27	920	34.0	795	5 O18394	O18394 drosophila
28	919	34.0	629	11 Q923N8	Q923n8 mus musculu
29	919	34.0	641	11 Q923N7	Q923n7 mus musculu
30	917.5	33.9	499	11 Q8VHH6	Q8vhh6 mus musculu
31	917	33.9	502	5 Q9N587	Q9n587 caenorhabdi
32	915	33.9	540	5 Q46134	Q46134 locusta mig
33	914.5	33.8	499	11 Q8R4G9	Q8r4g9 mus musculu
34	907	33.6	531	5 Q96632	Q96632 heliothis v
35	907	33.6	595	5 P91764	P91764 myzus persi
36	897.5	33.2	452	13 Q918C7	Q918c7 gallus gall
37	894	33.1	496	6 Q8SPU6	Q8spu6 bos taurus
38	894	33.1	533	5 Q8WRS1	Q8wrs1 chilo suppr
39	886	32.8	772	5 Q9W3G6	Q9w3g6 drosophila
40	885	32.7	776	5 Q44202	Q44202 drosophila
41	883.5	32.7	517	5 Q96633	Q96633 heliothis v
42	877	32.4	509	5 Q9NFX8	Q9nfx8 myzus persi
43	876.5	32.4	547	5 Q8WSF9	Q8wsf9 aplysia cal
44	876	32.4	497	5 Q46135	Q46135 locusta mig
45	874	32.3	494	11 Q9R0W9	Q9r0w9 mus musculu

ALIGNMENTS

RESULT 1

Q9JHD6 Q9JHD6 PRELIMINARY; PRT; 502 AA.
ID Q9JHD6;
AC Q9JHD6;
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
GN CHRNA7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21BG;
RX MEDLINE=97189245; PubMed=9037516;
RA Stitzel J.A., Farnham D.A., Collins A.C.;
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
restriction fragment length polymorphisms with levels of alpha-
bungarotoxin binding in brain."
RL Brain Res. Mol. Brain Res. 43:30-40(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21BG;
RX Submitted J.A.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AF225980; AAF35885.1; -.
DR MGD; MGI:99779; Chrna7.
DR InterPro; IPR00188; GABAA receptor.
DR MGD; MGI:99779; Chrna7.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;

KW Transmembrane.
 SQ SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;
 Query Match 94.2%; Score 2546; DB 11; Length 502;
 Best Local Similarity 93.8%; Pred. No. 3.2e-217;
 Matches 466; Conservative 19; Mismatches 12; Indels 0; Gaps 0;
 QY 6 GGWLALAAALHVSLLQGEFORLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
 DB 6 GGWLALAAALHVSLLQGEFORLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
 QY 66 DEKNQVLTNNIWMQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADDERFAT 125
 DB 66 DEKNQVLTNNIWMQSWTDHYLQWNVSEYPGVKNVRFDPGQIWKPDILLYNSADDERFAT 125
 QY 126 FHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOE 185
 DB 126 FHTNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOE 185
 QY 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLIS 245
 DB 186 DISSYIPNGEWDLVGIPGKRSERFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLIS 245
 QY 246 ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
 DB 246 ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVG 305
 QY 306 LSVVTVIVLYQHHPDGGKMPKTRVILLNWCWFLMRKRPGEQKVRPACQHKQRCS 365
 DB 306 LSVVTVIVLYQHHPDGGKMPKTRVILLNWCWFLMRKRPGEQKVRPACQHKQRCS 365
 QY 366 LASVENSAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLHGGQ 425
 DB 366 LASVELSAGAPSSNGNLLYIGRGLGHECAPDPSGVVCGRLACSPHDEHMGTH 425
 QY 426 PPEGDPDLAKILEBRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFIICTIG 485
 DB 426 PSDGDPDLAKILEBRYIANRFRQDESEVICSEWKFAACVVDRLCLMAFSVFIICTIG 485
 QY 486 ILMSAPNFVEAVSKDFA 502
 DB 486 ILMSAPNFVEAVSKDFA 502
 RESULT 2
 ID Q03481 PRELIMINARY; PRT; 511 AA.
 AC Q03481;
 DT 01-NOV-1996 (T-REMBLrel. 01, Created)
 DT 01-NOV-1996 (T-REMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (T-REMBLrel. 21, Last annotation update)
 DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=90315158; PubMed=2369519;
 RA Schoepfer R., Conroy W.G., Whiting P., Core M., Lindstrom J.;
 RT "Brain alpha-bungarotoxin-binding protein cDNAs and mAbs reveal
 subtypes of this branch of the ligand-gated ion channel gene
 superfamily.";
 RT Neuron 5:35-48(1990).
 RL Neuron 5:35-48(1990).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL; X52296; CAA36544.1;
 DR InterPro; IPR000188; GABA_A receptor.
 DR InterPro; IPR001175; Neur channel.
 DR Pfam; PF02931; Neur_chan_IAD; 1.
 DR Pfam; PF02932; Neur_chan_nemb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane. 1 30 POTENTIAL.
 FT SIGNAL 31 511 POTENTIAL.
 FT CHAIN
 SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;
 Query Match 67.2%; Score 1816.5; DB 13; Length 511;
 Best Local Similarity 68.8%; Pred. No. 1.6e-12;
 Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
 QY 8 VWLALAAALHVSLLQGEFORLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDVDE 67
 DB 16 LWASLFLSFPKVSQGESQRLYRDLRNYNLERPVANDSOPLTVYFSLSLQIMDVDE 75
 QY 68 KNOVLTNNIWMQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADDERFATFH 127
 DB 76 KNOVLTNNIWMQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADDERFATFH 135
 QY 128 TNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI 187
 DB 136 TNVLVNSGHCQYLPPIGIFKSSCYIDVRWFPDVOHCKLKFGSWSYGGWSLDLQOEADI 195
 QY 188 SGYIPNGEWDLVGIPGKRSERFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLISAL 247
 DB 196 SNYLSNGEWDLVGIPGKRSERFYECCKEYPDPDTFTVMRRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 307
 DB 256 ALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLS 315
 QY 308 VVTVIVLYQHHPDGGKMPKTRVILLNWCWFLMRKRPGEQKVRPACQHK--QRRC 364
 DB 316 VVTVIVLYQHHPDGGKMPKTRVILLNWCWFLMRKRPGEQKVRPACQHK--QRRC 374
 QY 365 SLASVENSAPPASNGNLLYIGRGLDGVHCVPTDPSGVVCGRMACSPHDEHLHGG 424
 DB 375 SLKNTMNVLPFGHGFSGNMIY-SYHTMENPCCQNDLGSKGKITPLSEDEHVKKK 433
 QY 425 QPPEGDPDLAKILEBRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFIICTI 484
 DB 434 ALMTIPVIVKILEVQFIANRFRQDEGEICSEWKFAAVIDRLCLVATFLFAICTF 493
 QY 485 GILMSAPNFVEAVSKDF 501
 DB 494 TILMSAPNFVEAVSKDF 510
 RESULT 3
 ID Q87TV5 PRELIMINARY; PRT; 807 AA.
 AC Q87TV5;
 DT 01-JUN-2002 (T-REMBLrel. 21, Created)
 DT 01-JUN-2002 (T-REMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-REMBLrel. 21, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha5 subunit.
 GN NACRALPHA-34E.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 Mediated A-to-I Pre-mRNA Editing";
 RT Genetics 160:1519-1533(2002).

[illegible]

RL Genet
DR'~ EMBL

Matches 234; Conservative 83; Mismatches 155; Indels 20; Gaps 6;

QY 10 LALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLILQIMDVDEKN 69
 DB 14 LLFLAIKESCOGPHKRLNHLSTYNTLERPVANSEPLEVKFGLTLOQIIDVDEKN 73
 QY 70 QVLTNWLQMSWDHYLQWNVSEYGVKTRFPDGOIWKPDILLYNSADERFDTHTN 129
 DB 74 QLLITNLWLSLEWNDYNLRNWEYEGGVKOLRITPNKLMKPDVLMYNSADEGFGDTHTN 133
 QY 130 VLNVSSGHCQYLPGIFKSSCYIDVRWFPDVOHCKLKFGWSYCGMSLDLQMOE---AD 186
 DB 74 QLLITNWLNLWNLNLRNWEYEGGVKOLRITPNKLMKPDVLMYNSADEGFGDTHTN 133
 QY 134 IVVKGSGCLYVPGIFKSTCKDITWFPDDQHCCKMFGSWYDGNQLDLVNSEDDGD 193
 QY 187 ISGYIPNGEWDLVGIPIGKRSERYECCKEYPDVFTVTRRRRTLYYGLNLLIPCVLISA 246
 DB 194 LSDFITNGEWYLLAMPKGNKTIYVACCEPEYVDITFTIQRRTLYYFNNLIVPCVLIS 253
 QY 247 LALLVLLPADSGEKISLIGTIVLLSTLTFMLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 DB 254 MALLGFTLPDPSGKLTGLVITLLSTVFNVAETLPQVSDAIPLLGTYFNCIMFMVAS 313
 QY 307 SVVTVIVLYQHHDHPDGGKMPKTRVILLNWCWFLRMKRPGEKVKRPACQHKORCSL 366
 DB 314 SVVLTVVLYNHHRTADIHMPPIKSVFLOLWPLWILRMGRPGKTRKTIILLNRMKEL 373
 QY 367 ASVEMSAVAPPASNGNLLYI--GFRGLDGVHCVPDTPDSGVVCGRMACSPT--HDEHLLH 422
 DB 374 ELKERS-----KSLIANVLIDDDFR-----HTISGQTAIGSSASFGRTTVEEHTAI 424
 QY 423 GGQPEGDPDLAKILEEVRIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTIIC 482
 DB 425 GC-----NHKDLHLKELQFITARMRKADDAELIGDWKFAAMVVDRCFLIVFTLFTIIA 480
 QY 483 TIGILMSAPNFV 494
 DB 481 TVTVLLSAPHII 492

RESULT 8
 Q8T7S1 PRELIMINARY; PRT; 494 AA.
 ID Q8T7S1
 AC Q8T7S1; 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type
 DE III.
 GN NACRALPHA-30D.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 RT Mediated A-to-I Pre-mRNA Editing.";
 RL Genetics 160:1519-1533 (2002).
 DR EMBL; AF321447; AAM13394.1; -.
 KW Receptor.
 SQ SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;

Query Match 44.9%; Score 1214; DB 5; Length 494;
 Best Local Similarity 47.4%; Pred. No. 3.9e-99;
 Matches 233; Conservative 84; Mismatches 155; Indels 20; Gaps 6;

QY 10 LALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLILQIMDVDEKN 69

DB 14 LLFLAIKESCOGPHKRLNHLSTYNTLERPVANSEPLEVKFGLTLOQIIDVDEKN 73
 QY 70 QVLTNWLQMSWDHYLQWNVSEYGVKTRFPDGOIWKPDILLYNSADERFDTHTN 129
 DB 74 QLLITNLWLSLEWNDYNLRNWEYEGGVKOLRITPNKLMKPDVLMYNSADEGFGDTHTN 133
 QY 130 VLNVSSGHCQYLPGIFKSSCYIDVRWFPDVOHCKLKFGWSYCGMSLDLQMOE---AD 186
 DB 134 IVVKGSGCLYVPGIFKSTCKDITWFPDDQHCCKMFGSWYDGNQLDLVNSEDDGD 193
 QY 187 ISGYIPNGEWDLVGIPIGKRSERYECCKEYPDVFTVTRRRRTLYYGLNLLIPCVLISA 246
 DB 194 LSDFITNGEWYLLAMPKGNKTIYVACCEPEYVDITFTIQRRTLYYFNNLIVPCVLIS 253
 QY 247 LALLVLLPADSGEKISLIGTIVLLSTLTFMLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 DB 254 MALLGFTLPDPSGKLTGLVITLLSTVFNVAETLPQVSDAIPLLGTYFNCIMFMVAS 313
 QY 307 SVVTVIVLYQHHDHPDGGKMPKTRVILLNWCWFLRMKRPGEKVKRPACQHKORCSL 366
 DB 314 SVVLTVVLYNHHRTADIHMPPIKSVFLOLWPLWILRMGRPGKTRKTIILLNRMKEL 373
 QY 367 ASVEMSAVAPPASNGNLLYI--GFRGLDGVHCVPDTPDSGVVCGRMACSPT--HDEHLLH 422
 DB 374 ELKERS-----KSLIANVLIDDDFR-----HTISGQTAIGSSASFGRTTVEEHTAI 424
 QY 423 GGQPEGDPDLAKILEEVRIANFRQDESEAVCEWKFACVVDRLCLMAFSVFTIIC 482
 DB 425 GC-----NHKDLHLKELQFITARMRKADDAELIGDWKFAAMVVDRCFLIVFTLFTIIA 480
 QY 483 TIGILMSAPNFV 494
 DB 481 TVTVLLSAPHII 492

RESULT 9
 Q8T7S0 PRELIMINARY; PRT; 509 AA.
 ID Q8T7S0
 AC Q8T7S0; 21, Created)
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type IV.
 GN NACRALPHA-30D.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21969411; PubMed=11973307;
 RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
 RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 RT Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
 RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
 RT Mediated A-to-I Pre-mRNA Editing.";
 RL Genetics 160:1519-1533 (2002).
 DR EMBL; AF321448; AAM13395.1; -.
 KW Receptor.
 SQ SEQUENCE 509 AA; 57887 MW; BE8D8E0198E0C2BD CRC64;

Query Match 44.6%; Score 1204.5; DB 5; Length 509;
 Best Local Similarity 46.2%; Pred. No. 2.8e-98;
 Matches 234; Conservative 84; Mismatches 154; Indels 35; Gaps 7;

QY 10 LALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLILQIMDVDEKN 69
 DB 14 LLFLAIKESCOGPHKRLNHLSTYNTLERPVANSEPLEVKFGLTLOQIIDVDEKN 73
 QY 70 QVLTNWLQMSWDHYLQWNVSEYGVKTRFPDGOIWKPDILLYNSADERFDTHTN 114
 DB 74 QLLITNWLNLWNLNLRNWEYEGGVKOLRITPNKLMKPDVLMYNSADEGFGDTHTN 133

QY	115	YNSADERFDATFHTNVLVNSSGHCOYLPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYG	174
Db	134	YNSADEGFDGTHTNIVKVRSGSLYVPPGIFKSTCKMDITWFPDDOHCMEKFGSWYD	193
QY	175	GWSLDLQMBE---ADISGYPNGBMDLVGIPGKRSERYECKBYPDVDTFTVNRRTL	231
Db	194	GNQJDLVLNSBEGDGLSDFITNGEWWLLAMPKKNITIVYACCPPEYVDITFIQIRRTL	253
QY	232	YYGNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLITFMLLVAEIMPATSDSPV	291
Db	254	YYFNLVLVPCVLISSMALLGFTLPDSGEKLTLGVTILLSTVFLNLVAETLPOVSDAIP	313
QY	292	LIAQYFASITLIVGLVVVTVIVLYQHHHDPDGGKMPKWTVRVILLNWCFLRMKRPGBD	351
Db	314	LLGTYNCFIMFWASSVVLTVVLYNHHRTADIHEMPPIKSVFLQWLPWILRMGRPGRK	373
QY	352	KVRPACQHKORRCSLASVEMSAVAPPASNGLLYI--GFRGLDGVHCVTPDPSGVWGR	409
Db	374	ITRKTILLSNRKELELKERSS---KSLLANVLIDDDFR-----HTISGSQTAIGSSA	424
QY	410	MACSPT--HDEHLLHGQOPPEGDPDLAKILBEVRYIANRFRQDSEAVCSWEKFAACVV	467
Db	425	SFRPTTVEEHHHTAIGC---NHKDLHLILKELQFITARMRKADDAEALIGDWKFAAMVV	480
QY	468	DRICLMAFSVPTIICTGILMSANFV	494
Db	481	DRFCLIVFTFTIATVTLVLSAPHII	507

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RESULT 10
Q8177R9
ID ID Q8T7R9 PRELIMINARY; PRT; 523 AA.
AC Q8T7R9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DE Nicotinic acetylcholine receptor Dalpha6 subunit variant V.
GN NACRALPHA-30D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
DR EMBL; AF321449; AAM13396.1; -.
KW Receptor.
SQ SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

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Qy	187	ISGYTPNGEWDLVGPGRKSERFYECCKEPYDPDVTVTWRRRTLYYGLNLLIPCVLISA	246
Db	194	LSDFITNGEYWLAMPKGNKNTIVACYCPPEFYVDITFIQIRRTLYYFFNLVPCVLISS	253
Qy	247	LALLVFLLPADGGEKISLIGITVLLSUTTFMLVAEIMPATSDSVPLI	293
Db	254	MALLGFTLPDGSGEKLTGLVTILLSTVFLNLVAESMPITSDAPLIGVTILLSLTVFLN	313
Qy	294	-----AQYFASMTIIVGLSVVVTVIVLYOHVHHDDPGGKMPKQKTRVILLN	337
Db	314	LVAETLPQVSDAIPLLIGTYFCINEMFVASSVLLTVVLNHYHRTADIHMPMPWIKSVFLQ	373
Qy	338	WCAPFLRMKRPGEDKVRPCAQHKQRCSLASVEMSAVAPPPASNGNLLYI--GFRGLDGV	395
Db	374	WLPWILRMGRPGRKITRKILLNRMKELEKERS-----KSLANVLIDDDDFR-----	424
Qy	396	HCVPTPDGSGVCGRMACSPT--HDEHLLHGQOPGEGDPLAKTILEEVRYIANFRCODES	453
Db	425	HTISGSQTAIGSSASFGRPRTTVEHHHTAIGC---NKHDLHLHLKLQFITARMRKADDE	480
Qy	454	EAVCSSEWKAACVVDRLCLIMAFSVFTIICITIGILMSAPNFV	494
Db	481	AEILGDWKAAMVVDRECLIVFTLFTLIATVTVLLSAPHII	521
RESULT 11			
O62083 PRELIMINARY; PRT; 554 AA.			
ID	O62083		
AC	O62083;		
DT	01-AUG-1998 (TrEMBLrel. 07, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)		
CS	C31H5.3 protein.		
GN	C31H5.3.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]-----		
RP	SEQUENCE FROM N.A.		
RA	Kershaw J.K.;		
RL	Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.		

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Db 247 ALLSFTLPADCGEKLNGVTFHSLCVFMIMVAEMPQTSALPLIQIFYFSCIMFQVGAS 306
QY 308 VVVTVIVLQVHHDDPGGK-MPKWTRVILLNWCAMFLMRKPPGDKVRPAQH-----K 360
Db 307 VVATVIALNPHRRSPQYKPMNKFLKTLILGWLPTLLGMRPDLVLELSVHGAYASDNKK 366
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLD-----393
Db 367 KORQYILIEVHERILTRP---NGN---GHSVADKAVHLDLSTGNPHSDAKKSSPKRSTS 419
QY 394 ----GVHCVPTP-----DSGV---VCGRMACGPTDHEHLLHGQPPGDDP-----431
Db 420 ASIMGWGTGLPTTQWNGALDSSINKYCTKVRPLENGSATINHKSQFQINNNNIYKC 479
QY 432 -----DLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRCLMAFSVFTI 480
Db 480 ANNOQTQFDRPHHILNELRVISARVKEEMHALQADNMFASRVVDRVCFLAFAFLF 539
QY 481 ICTIGILMSAPN 492
Db 540 MCTAIIISYNAPH 551

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RESULT 12

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P91197
ID P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.7 kDa protein.
GN D2092.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; U88167; AAB42223.1; -
DR InterPro; IPR001188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Hypothetical protein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 461 AA; 52718 MW; 6182A7F827357B92 CRC64;
Query Match 36.9%; Score 998; DB 5; Length 461;
Best Local Similarity 39.8%; Pred. No. 5.1e-80;

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Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;
QY 12 LAASLLHVL-OGFP-ORLYKLVKNYNPLRPVANDSQPLTVYFSLLLQIMVDEN 69
Db 10 LSLVIIHNLCDGSAETKLTDLKGYNPLRPVQNSQPLEVKIKLFLOQLDVEN 69
QY 70 QVLTNTIWLQSWTDHYLQWNVSEYGVKTVFRP--DGIWKPDILLNLSADDERDATEFH 127
Db 70 QIVSVNAWLSYTWFDHKLQWEPKYGIGQDIRFGSSDHIWKPDVLLYNAAEDFDSTPK 129
QY 128 TNVLVNSSGHCQYLPPIPGIFKSCYIDVRWFFDVQHCXKLFKGSWSYGSWLDLQW- 182
Db 130 SNLLTYHTGTVMTPPGVLKFCQDLVTFWFFDDOVCCKFGSWTFHGYAIDLQIDDDTN 189
QY 183 --QADISGYIPNGEWDLVGIPGRSERFYCKEPEYDPDVTVTMRRTLYYGLNLLIP 240
Db 190 GTQMDLSTYLVNGEWOIVSTNAKRVSVYKCCPEYPTVNYLHRRRTLYYGNLLIP 249
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVABIMPATSDSVLIAQYFAST 300
Db 250 SLLISLMAILGFMFPDAGEKITLEVITLLAIVFVFLSMVSEMTPTTSEAVPLIGVFFSC 309
QY 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCAMFLMRKPPGDKVRPAQH 360
Db 310 MLVVSASVFTIVVNLHFRSADSHENMPLVRRLEFLPMLFMRSGYKFKV-----363
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEH 419
Db 364 ----ANV-----IDSTDKMPKPKNPLDCLNLSNHAGYEAQ 395
QY 420 LHHGQPPGDDPLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRCLMAFSVFT 479
Db 396 ILL-----LHVSHTELRRVAVFYKNEHDERIQTDWRFAAMVVDRACLLLFTVFI 445
QY 480 ICTIGILMSAPNEV 494
Db 446 VISILAIMMSAPHII 460

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RESULT 13

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O46128
ID O46128 PRELIMINARY; PRT; 523 AA.
AC O46128;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha subunit precursor.
GN NACHR.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prorygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA JafariGorzini S., Maelicke A.;
RT "Preliminary: Cloning of nicotinic acetylcholine receptor subunits of
RT Heliothis virescens."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AJ000399; CAA04056.1; -
DR InterPro; IPR001188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00232; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 523 NICOTINIC ACETYLCHOLINE RECEPTOR.

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Search completed: June 20, 2003, 19:00:26
Job time : 89 secs

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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:57:06 ; Search time 27 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703
Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	502	4	US-08-771-737-2
2	2698	99.8	502	2	US-08-466-589-8
3	2698	99.8	502	2	US-08-700-636-8
4	2698	99.8	502	3	US-08-467-574-8
5	2698	99.8	502	4	US-09-217-345-8
6	2698	99.8	502	4	US-08-487-596-12
7	2540	94.0	502	1	US-08-278-635B-7
8	2540	94.0	502	3	US-08-464-258B-7
9	2540	94.0	502	3	US-08-471-961-7
10	1816.5	67.2	511	1	US-08-278-635B-8
11	1816.5	67.2	511	3	US-08-464-258B-8
12	1816.5	67.2	511	3	US-08-471-961-8
13	945	35.0	529	1	US-08-496-855A-2
14	945	35.0	529	4	US-08-487-596-2
15	943	34.9	510	1	US-08-278-635B-4
16	943	34.9	510	3	US-08-471-961-4
17	940.5	34.8	511	3	US-08-464-258B-4
18	920.5	34.1	528	2	US-08-466-589-2
19	920.5	34.1	528	3	US-08-700-636-2
20	920.5	34.1	528	3	US-08-467-574-2
21	920.5	34.1	528	4	US-09-217-345-2
22	908	33.6	504	2	US-08-466-589-4
23	908	33.6	504	2	US-08-700-636-4
24	908	33.6	504	3	US-08-467-574-4
25	908	33.6	504	4	US-09-217-345-4
26	905.5	33.5	629	1	US-08-278-635B-6
27	905.5	33.5	629	3	US-08-464-258B-6

28	905.5	33.5	629	3	US-08-471-961-6	Sequence 6, Appli
29	894	33.1	497	1	US-08-278-635B-5	Sequence 5, Appli
30	894	33.1	497	3	US-08-464-258B-5	Sequence 5, Appli
31	894	33.1	497	3	US-08-471-961-5	Sequence 5, Appli
32	887	32.8	627	4	US-08-487-596-6	Sequence 6, Appli
33	884	32.7	498	4	US-08-487-596-18	Sequence 18, Appli
34	882	32.6	504	4	US-08-487-596-4	Sequence 4, Appli
35	871	32.2	627	2	US-08-466-589-6	Sequence 6, Appli
36	871	32.2	627	3	US-08-700-636-6	Sequence 6, Appli
37	871	32.2	627	3	US-08-467-574-6	Sequence 6, Appli
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39	869	32.1	498	1	US-08-496-855A-6	Sequence 6, Appli
40	869	32.1	498	2	US-08-466-589-12	Sequence 12, Appli
41	869	32.1	498	2	US-08-700-636-12	Sequence 12, Appli
42	869	32.1	498	3	US-08-467-574-12	Sequence 12, Appli
43	869	32.1	498	4	US-09-217-345-12	Sequence 12, Appli
44	867.5	32.1	494	4	US-08-487-596-10	Sequence 10, Appli
45	861	31.9	502	2	US-08-466-589-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-771-737-2
; Sequence 2, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017 US 01
; CURRENT APPLICATION NUMBER: US/08/771,737
; CURRENT FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-08-771-737-2

Query Match	100.0%	Score	2703;	DB	4;	Length	502;
Best Local Similarity	100.0%	Pred. No.	4.6e-274;	Mismatches	0;	Indels	0;
Matches	502;	Conservative	0;	Gaps	0;		
Qy	1	MRCSPGGVWLALASLLHVS	QGFQKLYKELVKNYNPLRPVANDSOPLTVYFSLSL	60			
Db	1	MRCSPGGVWLALASLLHVS	QGFQKLYKELVKNYNPLRPVANDSOPLTVYFSLSL	60			
Qy	61	QIMDVEKNQVLTNNIWLQMSWTDHYLQWNSYEPGVKTVRFPDQIWKPDILLYNSADE	120				
Db	61	QIMDVEKNQVLTNNIWLQMSWTDHYLQWNSYEPGVKTVRFPDQIWKPDILLYNSADE	120				
Qy	121	RFDAFTFTNNLVNLSGHCQYLPFGIFKXSSCVIDVRWFDFVQHCKLKFGSWSGWSLDL	180				
Db	121	RFDAFTFTNNLVNLSGHCQYLPFGIFKXSSCVIDVRWFDFVQHCKLKFGSWSGWSLDL	180				
Qy	181	QMQADISGYTPNGEWDLVGPGRKSERFYCCKEPYEDVTFTVMRRRTLYYGNLLIP	240				
Db	181	QMQADISGYTPNGEWDLVGPGRKSERFYCCKEPYEDVTFTVMRRRTLYYGNLLIP	240				
Qy	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300				
Db	241	CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300				

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 Db 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPBGDKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-08-466-589-8
 ; Sequence 8, Application US/08466589
 ; Patent No. 5837489
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClaim
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,589
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: March 8, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9950
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-466-589-8

Query Match 99.8%; Score 2698; DB 2; Length 502;
 Best Local Similarity 99.8%; Pred. No. 1.5e-273;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWALAAASLHVSLQGEFQRLKYELVKNYNPLRPVANDSQPLTVVFSLSLL 60
 Db 1 MRCSPGGVWALAAASLHVSLQGEFQRLKYELVKNYNPLRPVANDSQPLTVVFSLSLL 60
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Db 61 QINDVDEKNQVLTNWLQMSWTDHYLQMNVSYPGVKTRVFPDQGIWKPDILLYNSADE 120
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 Db 121 RFDATHTNVLNVSNGHCQYLPGIFKSSCVIVRWPFDFVQHCCKLFGWSYGGWSL 180
 QY 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYPDVTFVTMRRRTLYYGLNLLIP 240
 Db 181 QMOEADISGYIPNGEWDLVGIPGKRSEFYECCKEPEYPDVTFVTMRRRTLYYGLNLLIP 240
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 Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPBGDKVRPACQHK 360
 Db 301 MIIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPBGDKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-08-700-636-8
 ; Sequence 8, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
US-08-700-636-8

Query Match 99.8%; Score 2698; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
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DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
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DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
QY 421 LHGGQPEGPDPAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGPDPAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704

GENERAL INFORMATION:

;; APPLICANT: Elliot, Kathryn J.
;; APPLICANT: Ellis, Steven B.
;; APPLICANT: Harpold, Michael M.
;; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Brown, Martin, Haller & McClaim
;; STREET: 1660 Union Street
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/467,574
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/028,031
;; FILING DATE: March 8, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-9949
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-238-0999
;; TELEFAX: 619-238-0062
;; TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

;; LENGTH: 502 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: unknown

;; MOLECULE TYPE: protein

US-08-467-574-8

Query Match 99.8%; Score 2698; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-273;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
DB 1 MRCSPGGVWLAALASLLHVSILQGFQKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
QY 61 QIMDVDEKNOVLTNINLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
DB 61 QIMDVDEKNOVLTNINLQMSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
QY 121 RFDAFTHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
DB 121 RFDAFTHTNVLNVSNGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLYQHHDDPGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVIVLYQHHDDPGKMPKTRVILLNCAWFLMRKRPGEKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGMACSPTHDEHL 420
QY 421 LHGGQPEGPDPAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGPDPAKILEEVRYIANFRQCDESAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-09-217-345-8
; Sequence 8, Application US/09217345
; Patent No. 6303753

GENERAL INFORMATION:

;; APPLICANT: Elliot, Kathryn J.
;; APPLICANT: Ellis, Steven B.
;; APPLICANT: Harpold, Michael M.
;; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US/09/217,345
APPLICATION NUMBER: US/09/217,345
FILING DATE: 21-DEC-98
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,574
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/466,589,
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9949B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-217-345-8

Query Match	99.8%;	Score 2698;	DB 4;	Length 502;
Best Local Similarity	99.8%;	Pred. No. 1.5e-273;		
Matches 501;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MRCSPGGVWLALAAALLHVLSLQGEFQRLKYKELVKNYNPLRPVANDSQPLTVVFSLSLL	60	
Db	1	MRCSPGGVWLALAAALLHVLSLQGEFQRLKYKELVKNYNPLRPVANDSQPLTVVFSLSLL	60	
QY	61	QIMDVDEKNQVLTNNIWLQMSWTDHYILOWNVSEYPGVKTVPDQGIWKPDILLVNSADE	120	
Db	61	QIMDVDEKNQVLTNNIWLQMSWTDHYILOWNVSEYPGVKTVPDQGIWKPDILLVNSADE	120	
QY	121	RFDATFHTNVLVNSSGHCQYLPDGI FKSSCSYIDVRWPPFDVQHCKLKFGSWSYGGWSLDDL	180	
Db	121	RFDATFHTNVLVNSSGHCQYLPDGI FKSSCSYIDVRWPPFDVQHCKLKFGSWSYGGWSLDDL	180	
QY	181	QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPPYDPDVTFTVTMRRTLLVYGNLLIIP	240	
Db	181	QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPPYDPDVTFTVTMRRTLLVYGNLLIIP	240	
QY	241	CVLISALALAVFLLPADSGEKISIGITVLLSLTTFMLLVAAETMPATSDSVPLIAQVFAST	300	
Db	241	CVLISALALAVFLLPADSGEKISIGITVLLSLTTFMLLVAAETMPATSDSVPLIAQVFAST	300	
QY	301	MIIVGLSVVTVTVIQLQVHHHPDGGCKMPKWTRVILLNNCAWFLRMKRPGEDKVRPACQHK	360	
Db	301	MIIVGLSVVTVTVIQLQVHHHPDGGCKMPKWTRVILLNNCAWFLRMKRPGEDKVRPACQHK	360	
QY	361	QRRCSLASVEMSAVAPPASNGNLLYIGFGRLDGVHCVPTDPSGVVCGEMACSPTHDEHL	420	
Db	361	QRRCSLASVEMSAVAPPASNGNLLYIGFGRLDGVHCVPTDPSGVVCGEMACSPTHDEHL	420	
QY	421	LHGQPPGEGDPLAKILIEEVRYIANRFRQDESEAVCSSEWTFPAAACVWRRLCIAMAFSVFTI	480	

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Db 421 LHGGOPPGDPLAKILEVRYIANRFRCODESEAVCEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
US-08-487-596-12
: Sequence 12, Application US/08487596
: Patent No 6440681
: GENERAL INFORMATION:
: APPLICANT: Elliot, Kathryn J.
: APPLICANT: Ellis, Steven B.
: APPLICANT: Harpold, Michael M.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
: TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
: TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Brown, Martin, Hallier & McClain
: STREET: 1660 Union Street
: CITY: San Diego
: STATE: CA
: COUNTRY: USA
: ZIP: 92101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,596
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO US94/02447
: FILING DATE: 08-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/149,503
: FILING DATE: 08-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/028,031
: FILING DATE: 08-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/938,154
: FILING DATE: 30-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/504,455
: FILING DATE: 03-APR-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Seidman, Stephanie L.
: REGISTRATION NUMBER: 33,779
: REFERENCE/DOCKET NUMBER: 6362-9951
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-238-0999
: TELEFAX: 619-238-0062
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 502 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
US-08-487-596-12

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	Query Match	99.8%	Score 2698;	DB 4;	Length 502;
	Best Local Similarity	99.8%;	Pred. No. 1.5e-273;		
	Matches 501; Conservative	0;	Mismatches 1;	Indels	0; Gaps
Qy	1	MRCSGGWGLAASLLHVS	LQGEFORKYKELVKNINPLRPVANDSQPLTVTFESLSL	60	
Db	1	MRCSGGWGLAASLLHVS	LQGEFORKYKELVKNINPLRPVANDSQPLTVTFESLSL	60	

Qy	61	QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGOIKWPKDILLVNSADE	120
Db	61	QIMDVDEKNQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTVRPPDGOIKWPKDILLVNSADE	120
Qy	121	RFDATFHTNNVLVNSSGHCQOYLPPGIFKSSCYIDVRWPFEDVQCHLKFQMSYSGWSLDL	180
Db	121	RFDATFHTNNVLVNSSGHCQOYLPPGIFKSSCYIDVRWPFEDVQCHLKFQMSYSGWSLDL	180
Qy	181	QMQRADISGYIPNGSBDLVGIPGKSESEFYECCKEPPYPDVTFTVMRRRTLYYGLNLLIP	240
Db	181	QMQRADISGYIPNGSBDLVGIPGKSESEFYECCKEPPYPDVTFTVMRRRTLYYGLNLLIP	240
Qy	241	CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Db	241	CVLISALALLVFLPADSGEKISLGITVLLSTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Qy	301	MIIVGLSVVTVTVIQLYHHHDPDGGKMPKWTREVILLNCWAFELMKRCGEDKVRPACQHK	360
Db	301	MIIVGLSVVTVTVIQLYHHHDPDGGKMPKWTREVILLNCWAFELMKRCGEDKVRPACQHK	360
Qy	361	QRRCSLASVENSASAVAPPASNGNLLIYIGRGLDGVHCVPTPDGSGVCGRMACSPHDEHL	420
Db	361	QRRCSLASVENSASAVAPPASNGNLLIYIGRGLDGVHCVPTPDGSGVCGRMACSPHDEHL	420
Qy	421	LHGQPPPEGDDPLAKILEEVRYIANRFRQDESEAVCSSEWKFAACVVDRLCLMAFSVFTI	480
Db	421	LHGQPPPEGDDPLAKILEEVRYIANRFRQDESEAVCSSEWKFAACVVDRLCLMAFSVFTI	480
Qy	481	ICTIGILMSAPNFVEAVSKDFA	502
Db	481	ICTIGILMSAPNFVEAVSKDFA	502

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7

Query Match          94.0%; Score 2540; DB 1; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0

Qy 6 GGVWLAALAAALLHVSLOGEPORKLYKELVKNYNPLERPVANDSQBLTVYFVSLSLQIMDV 65
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Db 6 GGIWLAALAAALLHVSLOGEFORRLYKELVKNYNPLERPVANDSQBLTVYFVSLSLQIMDV 65
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Qy 66 DEKNQVLTTNIWLQMSWTDHYLQWNVSYPGVKTVRFPDGGQIWKPDILLYNSADERFDAT 125
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 66 DEKNQVLTTNIWLQMSWTDHYLQWNVSYPGVKTVRFPDGGQIWKPDILLYNSADERFDAT 125
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Qy 126 FHTNVLNNSGHCQYLPPIFKSSCYIDVRFPDPVQHKLFKGSWSYGGWSLDLQMGBA 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 126 FHTNVLNNSGHCQYLPPIFKSSCYIDVRFPDPVQHKLFKGSWSYGGWSLDLQMGBA 185
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEPYDPVTFVTMRRRTLYYGLNLLIPCVLIS 245
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 186 DISSYIPNGEWDLVGIPGKRNKEFYECCKEYPDVTVTVMRRRTLYYGLNLLIPCVLIS 245
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 246 ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPPLIAQIPASTMIIVG 305
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 ALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPPLIAQIPASTMIIVG 305
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 306 LSVVTVTVILQYHHHDPDGGKMPKWTIRVILLNWCWAFURMKRPGEDKVRPACQHKRRC 365
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 LSVVTVTVILRYHHHDPDGGKMPKWTIRVILLNWCWAFURMKRPGEDKVRPACQHKRRC 365
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 366 LASVEMSAVAPPASNGNLLYIGRGLDGVHCVTPDSDSGVVCGRMACSPTHDEHLHGQ 425
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 366 LASVELSAGAPPTNSGNLLYIGRGLGEMHCATPDSGVVCGRMACSPTHDEHLMHGHA 425
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 426 PPEGDPDLAKILEVRVIANFRQDSSEAVCSWKFAACVVDRLCLMAFSVFTTICTIG 485
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 426 PSDGDPDLAKILEVRVIANFRQDSSEVICSEWKFAACVVDRLCLMAFSVFTTICTIG 485
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 486 ILSAPNFVEAVSKDPA 502
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 486 ILSAPNFVEAVSKDPA 502
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530

```

;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-2588-7

STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-7

Query Match 94.0%; Score 2540; DB 3; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGWLALAAALLHVSLSQGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
DB 6 GGIWLAALAAALLHVSLSQGEFORRLLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPDPGQIWKPDILLYNSADERFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPDPGQIWKPDILLYNSADERFDAT 125
QY 126 FHTNVLNASSGHCOYLPPGIFKSSCYIDVRWFPDVQCKLKFGSWSYGGWSLDLQMOEA 185
DB 126 FHTNVLNASSGHCOYLPPGIFKSSCYIDVRWFPDVQCKLKFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
QY 186 DISSYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
DB 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
QY 306 LSVVVTVIVLYHHHPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHKQRRC 365
DB 306 LSVVVTVIVLYHHHPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHKQRRC 365
QY 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPDTPDSGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAGPPTSGNLLYIGRGLDGVHCVPDTPDSGVVCGRMACSPTHDEHLHGQ 425
QY 426 PPGDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRCLCLMAFSVFTICTIG 485
DB 426 PSDGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRCLCLMAFSVFTICTIG 485
QY 486 ILMGAPNFVEAVSKDFA 502
DB 486 ILMGAPNFVEAVSKDFA 502

RESULT 9
US-08-471-961-7
; Sequence 7, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH

Query Match 94.0%; Score 2540; DB 3; Length 502;
Best Local Similarity 93.6%; Pred. No. 5.2e-257;
Matches 465; Conservative 18; Mismatches 14; Indels 0; Gaps 0;

QY 6 GGWLALAAALLHVSLSQGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
DB 6 GGIWLAALAAALLHVSLSQGEFORRLLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPDPGQIWKPDILLYNSADERFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQNMVSEYPGVKTVRPDPGQIWKPDILLYNSADERFDAT 125
QY 126 FHTNVLNASSGHCOYLPPGIFKSSCYIDVRWFPDVQCKLKFGSWSYGGWSLDLQMOEA 185
DB 126 FHTNVLNASSGHCOYLPPGIFKSSCYIDVRWFPDVQCKLKFGSWSYGGWSLDLQMOEA 185
QY 186 DISGYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPGKRSEYFECCKEPYDPVTVTVMRRRTLYYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
DB 246 ALALLVFLPADSGEKISLGTIVLLSLTTFMLVAEIMPATSDSVPLIAQYFASFTMIIVG 305
QY 306 LSVVVTVIVLYHHHPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHKQRRC 365
DB 306 LSVVVTVIVLYHHHPDGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHKQRRC 365
QY 366 LASVMSAVAPPASNGNLLYIGRGLDGVHCVPDTPDSGVVCGRMACSPTHDEHLHGQ 425
DB 366 LASVELSAGAGPPTSGNLLYIGRGLDGVHCVPDTPDSGVVCGRMACSPTHDEHLHGQ 425
QY 426 PPGDPLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRCLCLMAFSVFTICTIG 485
DB 426 PSDGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRCLCLMAFSVFTICTIG 485
QY 486 ILMGAPNFVEAVSKDFA 502
DB 486 ILMGAPNFVEAVSKDFA 502

QY 188 SGYIPNGEWDLVGPGRSERFECCKEYKELVKNYNPLERPVANDSQPLTVVFSLSLQIMDYDE 247
 DB 196 SNYISNGEWDLVGPGRNELYECCKEYKELVKNYNPLERPVANDSQPLTVVFSLSLQIMDYDE 255
 QY 248 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
 DB 256 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
 QY 308 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 364
 DB 316 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGG 424
 DB 375 SLKNTMNVLPQHPSNGNMIY-SYHTMENPCCPNNDLGSKSGKITCPLSEDNEHVQKK 433
 QY 425 QPPEGDPDLAKILEEVRYIANRRCQDESEAVCSWKFACVVDRLCLMAFVSFTIICTI 484
 DB 434 ALMDTIPVIVKILEEVQFIAMRFRKQDEGEICSEWKFACVVDRLCLMAFVSFTIICTF 493
 QY 485 GILMSAPNFIEAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510

RESULT 12
 US-08-471-961-8
 ; Sequence 8, Application US/08471961
 ; Patent No. 6100046
 ; GENERAL INFORMATION:
 ; APPLICANT: ELGOYHEN, ANA BELEN
 ; APPLICANT: JOHNSON, DAVID S.
 ; APPLICANT: BOULTER, JAMES R.
 ; APPLICANT: HEINEMANN, STEPHEN F.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 ; TITLE OF INVENTION: ACETYLCOLINE-GATED ION CHANNEL RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 ; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,961
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/278,635
 ; FILING DATE: 21-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REITER, STEPHEN E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-677-1409
 ; TELEFAX: 619-677-1465
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 511 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-471-961-8

Query Match 67.2%; Score 1816.5; DB 3; Length 511;
 Best Local Similarity 68.8%; Pred. No. 2.6e-181;

Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
 QY 8 VWLALAAASLLHVSLSQGEFORKLYKELVKNYNPLERPVANDSQPLTVVFSLSLQIMDYDE 67
 DB 16 LWASLFLSFFKVSQGESQRLYEDLLRNYNRLERPVANDSQPIVVELQSLQIIDVDE 75
 QY 68 KNOVLTNNIWLQMSWTDHYLQWNVSEYGPVKTVPFDPGQIWKPDILLVNSADERPDATFH 127
 DB 76 KNOVLTNNIWLQMSWTDHYLQWNVSEYGPVKTVPFDPGQIWKPDILLVNSADERPDATFH 135
 QY 128 TNVLVNSSGHCOYLPGRIFKSSCYIDVRWPPFDVQHCCKLKEGSSYSGWSLDLOMQEADI 187
 DB 136 TNVLVNSSGHCOYLPGRIFKSSCYIDVRWPPFDVQHCCKLKEGSSYSGWSLDLOMQEADI 195
 QY 188 SGYIPNGEWDLVGPGRSERFECCKEYKELVKNYNPLERPVANDSQPLTVVFSLSLQIMDYDE 247
 DB 196 SNYISNGEWDLVGPGRNELYECCKEYKELVKNYNPLERPVANDSQPLTVVFSLSLQIMDYDE 255
 QY 248 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 307
 DB 256 ALLVFLPADSGEKISLIGITVLLSLTFMMLVAEIMPATSDSVPLIAQYFASIMVIGLS 315
 QY 308 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 364
 DB 316 VVTVIVLVQHHHDPDGGKMPKTRVILLNWCWFLRMKRPGEKVRP-ACQHK--QRRK 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTDPSGVVCGRMACSPTHDEHLLHGG 424
 DB 375 SLKNTMNVLPQHPSNGNMIY-SYHTMENPCCPNNDLGSKSGKITCPLSEDNEHVQKK 433
 QY 425 QPPEGDPDLAKILEEVRYIANRRCQDESEAVCSWKFACVVDRLCLMAFVSFTIICTI 484
 DB 434 ALMDTIPVIVKILEEVQFIAMRFRKQDEGEICSEWKFACVVDRLCLMAFVSFTIICTF 493
 QY 485 GILMSAPNFIEAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510

RESULT 13
 US-08-496-855A-2
 ; Sequence 2, Application US/08496855A
 ; Patent No. 5801232
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/496,855A
 ; FILING DATE: 20-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/149,503
 ; FILING DATE: 08-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie

```

; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9369B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-496-855A-2

Query Match      35.0%; Score 945; DB 1; Length 529;
Best Local Similarity 39.8%; Pred. No. 4.1e-90;
Matches 200; Conservative 78; Mismatches 160; Indels 64; Gaps 9;

QY 24 EFQKLYKELVKNYPLRPVANDSQPLTVVYFSLQLQIMDVDEKNQVLTNNIQLQMSWT 83
DB 57 ETEDRLEFKHLFRGYNRWARPVNTSDVVIVRFGLSIAQLIDVDEKNQMTNNVWLKQWS 116
QY 84 DHYLQNVSEYPGVKTFRFDPGQIWKPDILLYNSADERFDATFTTNVLVNSGHCQYLPP 143
DB 117 DYKLRNPNADFGNITSLRVSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVHWVPP 176
QY 144 GIFKSSCYIDVRWFPFDVQHKLKFGSWSYGGWLDLQMQE--ADISGYIPNGEWDLVGI 201
DB 177 AIYKSSCSIDVTFPPDQONCKMFGSWTYDKAKIDLEQMEQTVDLKDYWESGEWAIYNA 236
QY 202 PGKRSERFECCKEPPDVTFTVMRRRTLYYGNLILPCVLISALALLVFLPADSGEK 261
DB 237 TGTYSKKYDCCAEIYPDVTYAFVIRLPLFYTNILIPCLLISCLTVLFPYLPSCGCK 296
QY 262 ISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASTMIIVGLSVVTVIVLQYHHHD 321
DB 297 ITCISVLLSLTVFLLITELIIPSTSLVPLIGEYLLFTWIFVLSIVITVFLNVHRS 356
QY 322 PDGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCRCSLASVEMSAVAPPPASN 381
DB 357 PSTHTMPHWVRGALLGCVPRWLLMNRP-----PPVEL 389
QY 382 GNLLYI-----GFRGLD-----VHCVPDPSGVVCGRMA-----CSPTHDEHLLHGG 424
DB 390 CHPLRLKLSPSYHWLESNDABEREVVVEEDRWACAGHVAPSVTGLCSHG-----LHSG 445
QY 425 QP-----PEGD-----PDLAKILEVRVYIANFRFCODESEAVCSWKFAACVVDRLCL 472
DB 446 ASGPKAELLOEGELLSPHQKALEGVHYIAHLRSEDADSSVKEDWKYVAMVIDRIFL 505
QY 473 MAFSVFTIICTIGILMSAPNFV 494
DB 506 WLFIIVCFLGTIGLFL--PPFL 525

RESULT 14
US-08-487-596-2
; Sequence 2, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; NUMBER OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101

```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-596-2

Query Match      35.0%; Score 945; DB 4; Length 529;
Best Local Similarity 39.8%; Pred. No. 4.1e-90;
Matches 200; Conservative 78; Mismatches 160; Indels 64; Gaps 9;

QY 24 EFQKLYKELVKNYPLRPVANDSQPLTVVYFSLQLQIMDVDEKNQVLTNNIQLQMSWT 83
DB 57 ETEDRLEFKHLFRGYNRWARPVNTSDVVIVRFGLSIAQLIDVDEKNQMTNNVWLKQWS 116
QY 84 DHYLQNVSEYPGVKTFRFDPGQIWKPDILLYNSADERFDATFTTNVLVNSGHCQYLPP 143
DB 117 DYKLRNPNADFGNITSLRVSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVHWVPP 176
QY 144 GIFKSSCYIDVRWFPFDVQHKLKFGSWSYGGWLDLQMQE--ADISGYIPNGEWDLVGI 201
DB 177 AIYKSSCSIDVTFPPDQONCKMFGSWTYDKAKIDLEQMEQTVDLKDYWESGEWAIYNA 236
QY 202 PGKRSERFECCKEPPDVTFTVMRRRTLYYGNLILPCVLISALALLVFLPADSGEK 261
DB 237 TGTYSKKYDCCAEIYPDVTYAFVIRLPLFYTNILIPCLLISCLTVLFPYLPSCGCK 296
QY 262 ISLGITVLLSLTTFMLLVAEIMPATSDVPLIAQYFASTMIIVGLSVVTVIVLQYHHHD 321
DB 297 ITCISVLLSLTVFLLITELIIPSTSLVPLIGEYLLFTWIFVLSIVITVFLNVHRS 356
QY 322 PDGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQHKQRCRCSLASVEMSAVAPPPASN 381
DB 357 PSTHTMPHWVRGALLGCVPRWLLMNRP-----PPVEL 389
QY 382 GNLLYI-----GFRGLD-----VHCVPDPSGVVCGRMA-----CSPTHDEHLLHGG 424
DB 390 CHPLRLKLSPSYHWLESNDABEREVVVEEDRWACAGHVAPSVTGLCSHG-----LHSG 445
QY 425 QP-----PEGD-----PDLAKILEVRVYIANFRFCODESEAVCSWKFAACVVDRLCL 472

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Db 446 ASGPKEALLQEGELLSPHQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRFL 505

QY 473 MAFSVFTIITIGILMSAPNFV 494

Db 506 WLFIIIVCFGLTIGLFL--PPFL 525

RESULT 15

US-08-278-635B-4
 ; Sequence 4, Application US/08278635B
 ; Patent No. 5683912
 ; GENERAL INFORMATION:
 ; APPLICANT: ELGOYHEN, ANA BELEN
 ; APPLICANT: JOHNSON, DAVID S.
 ; APPLICANT: BOULTER, JAMES R.
 ; APPLICANT: HEINEMANN, STEPHEN F.
 ; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 ; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 ; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/278,635B
 ; FILING DATE: 21-JUL-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REITER, STEPHEN E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9771
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-677-1409
 ; TELEFAX: 619-677-1465
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 510 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-278-635B-4

Query Match 34.9%; Score 943; DB 1; Length 510;
 Best Local Similarity 39.0%; Pred. No. 6.2e-90;
 Matches 201; Conservative 83; Mismatches 178; Indels 54; Gaps 9;
 QY 8 VW--LALAASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYVPSLSLLQIMDV 65
 Db 16 LWCLLLVPAVLTOQGSHTAEDRLFKHFGGYNRWARPVNTSDVIVRFGLSIAQLIDV 75
 QY 66 DEKNQVLTINILQMSQTDHYLOWNVSEYPGVKTVPDPGQIWKPKDILLVNSADERFDAT 125
 Db 76 DEKNQMTTNVWLKQENDYNVRDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGEPAVT 135
 QY 126 FHTNVLVNSGHCOYLPPIGPKSSCYIDRVFPDPVQHKCLKPGSWSYGGWSLDLQMOE- 184
 Db 136 HMTKAHLFFGTGVHVPVPAIYKSSCSIDVTFPPDQCKMKFGSWTYDKAKIDLEQMER 195
 QY 185 -ADISGYPNGENDLVGPKGRSERFYECKPEYDPDVTFTVTRRTLYYGLNLLIPCVL 243
 Db 196 TVDLKDYWESGEWAINATGYNSKKYDCCAEIYDPDVTYTVFVIRRLPLFTINLIICLL 255
 QY 244 ISALALIVFLPADSGEKISIGITVLSLTTFMLLVABIMPATSDSVPLIAQYFASTMI 303
 Db 256 ISCLTVLVFVLPSECGEKITICISVLSLTVFLVLLITELIIPSTSLVIFLIGEYLLFTWIF 315

QY 304 VGLSVVVTVIYVLYHHDDPDGGRMPKWTRVILLNWCWFLRMKRP-----GEDKVRPA 356
 Db 316 VTLISIVITVFLVNVHRSRSPSTHNNPNNVVRVALLGRVPRWLMNRPPLPPMELHGSPLDKLS 375
 QY 357 CQHKQRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDS--GVVCGRMACSP 414
 Db 376 PSYHWLETNMDAGEREETEEEEEDENICV-----CAGLPDSSMGVLYG----- 419
 QY 415 THDEHLLHGG-----QPPEG-----DPDLAKILEEVRYTIANRFRCODESEAVCS 458
 Db 420 -----HGGHLHRAPEFTKTPSQASEILLSPQIKALEGVHYIADHLRSEDADSSVKE 472
 QY 459 EWKFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494
 Db 473 DWKYVAMVVDRIFLWLFIIIVCFGLTIGLFL--PPFL 506

Search completed: June 20, 2003, 19:01:50
 Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:10:22 ; Search time 27 Seconds
(without alignments)
547.048 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGVWLALASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 6

Total number of hits satisfying chosen parameters: 766

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	502	100.0	502	US-08-771-737-2	Sequence 2, Appli
2	401	79.9	502	US-08-466-589-8	Sequence 8, Appli
3	401	79.9	502	US-08-700-636-8	Sequence 8, Appli
4	401	79.9	502	US-08-467-574-8	Sequence 8, Appli
5	401	79.9	502	US-09-217-345-8	Sequence 8, Appli
6	401	79.9	502	US-08-487-596-12	Sequence 12, Appli
7	62	12.4	502	US-08-278-635B-7	Sequence 7, Appli
8	62	12.4	502	US-08-464-258B-7	Sequence 7, Appli
9	62	12.4	502	US-08-471-961-7	Sequence 7, Appli
10	27	5.4	511	US-08-278-635B-8	Sequence 8, Appli
11	27	5.4	511	US-08-464-258B-8	Sequence 8, Appli
12	27	5.4	511	US-08-471-961-8	Sequence 8, Appli
13	10	2.0	479	US-08-278-635B-2	Sequence 2, Appli
14	10	2.0	479	US-08-464-258B-2	Sequence 2, Appli
15	10	2.0	479	US-08-471-961-2	Sequence 2, Appli
16	8	1.6	141	US-07-695-564-5	Sequence 5, Appli
17	8	1.6	141	US-08-241-387-5	Sequence 5, Appli
18	8	1.6	149	US-07-695-564-7	Sequence 7, Appli
19	8	1.6	149	US-08-241-387-7	Sequence 7, Appli
20	7	1.4	29	US-09-227-357-184	Sequence 184, App
21	7	1.4	37	US-09-227-357-399	Sequence 399, App
22	7	1.4	73	US-08-997-080-141	Sequence 141, App
23	7	1.4	73	US-08-997-362-141	Sequence 141, App
24	7	1.4	73	US-09-095-855-141	Sequence 141, App
25	7	1.4	73	US-09-324-542-141	Sequence 141, App
26	7	1.4	73	US-09-205-426-141	Sequence 141, App
27	7	1.4	157	US-08-164-292B-4	Sequence 4, Appli

28	7	1.4	157	3	US-08-845-623-4	Sequence 4, Appli
29	7	1.4	157	3	US-08-815-927-4	Sequence 4, Appli
30	7	1.4	157	4	US-09-103-330-4	Sequence 4, Appli
31	7	1.4	157	4	US-09-435-242-4	Sequence 4, Appli
32	7	1.4	174	2	US-08-683-262B-45	Sequence 45, Appli
33	7	1.4	174	2	US-08-683-262B-48	Sequence 48, Appli
34	7	1.4	174	3	US-09-122-443-6	Sequence 6, Appli
35	7	1.4	174	4	US-09-361-707-45	Sequence 45, Appli
36	7	1.4	174	4	US-09-361-707-48	Sequence 48, Appli
37	7	1.4	183	4	US-09-615-192A-303	Sequence 303, App
38	7	1.4	261	4	US-09-134-001C-4966	Sequence 4966, Ap
39	7	1.4	268	4	US-09-383-586-14	Sequence 14, Appli
40	7	1.4	331	2	US-08-997-080-182	Sequence 182, App
41	7	1.4	331	2	US-08-997-362-182	Sequence 182, App
42	7	1.4	331	4	US-09-095-855-182	Sequence 182, App
43	7	1.4	331	4	US-09-324-542-182	Sequence 182, App
44	7	1.4	331	4	US-09-205-426-182	Sequence 182, App
45	7	1.4	352	4	US-09-576-160B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-771-737-2
; Sequence 2, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017 US.01
; CURRENT APPLICATION NUMBER: US/08/771,737
; CURRENT FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-08-771-737-2

Query Match 100.0%; Score 502; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRCSPGGVWLALASLLHVS	100.0%	QYKLYKELVKNVKNPLRPVANDSQPLTVYFSL	60
Db	1	MRCSPGGVWLALASLLHVS	100.0%	QYKLYKELVKNVKNPLRPVANDSQPLTVYFSL	60
Qy	61	QIMVDKKNQVLTNIWLQMSWTDHYLQWNSVSEPGVKTVPFPGQIWKPDILLYNSADE	120		
Db	61	QIMVDKKNQVLTNIWLQMSWTDHYLQWNSVSEPGVKTVPFPGQIWKPDILLYNSADE	120		
Qy	121	RFDAFTHNVLSNGHCOYLPFGIFKSSCYDVRWPFVDVQHCKLKEGWSYGSWGLDL	180		
Db	121	RFDAFTHNVLSNGHCOYLPFGIFKSSCYDVRWPFVDVQHCKLKEGWSYGSWGLDL	180		
Qy	181	QMQRADISGYIPNGEWDLVGIPGKRSEFYECCKEPYPDVFTVTMRRTLYYGLNLLIP	240		
Db	181	QMQRADISGYIPNGEWDLVGIPGKRSEFYECCKEPYPDVFTVTMRRTLYYGLNLLIP	240		
Qy	241	CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVFLIAQYFAST	300		
Db	241	CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDSVFLIAQYFAST	300		

QY 301 MIIVGLSVVTVTVIQLYHHDDPGKPKWTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVTVIQLYHHDDPGKPKWTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-08-466-589-8
 ; Sequence 8, Application US/08466589
 ; Patent No. 5837489
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & Mcclain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION NUMBER: US/08/466,589
 ; FILING DATE: June 5, 1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: March 8, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9950
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-466-589-8

Query Match 79.9%; Score 401; DB 2; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches: 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 Db 1 MRCSPGGVWLAAASLLHVSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY .61 QIMDVDEKQVLTNIWLQSWTHYLQWNVSEYPGVKTRFPDQGIWKPDILLYNSADE 120

Db 61 QIMDVDEKQVLTNIWLQSWTHYLQWNVSEYPGVKTRFPDQGIWKPDILLYNSADE 120
 QY 121 RFQATHTNVLNVSNGHCOYLPPGIFKSSCYIDVRWFFPDVQHCCKLFGWSYGSLSL 180
 Db 121 RFQATHTNVLNVSNGHCOYLPPGIFKSSCYIDVRWFFPDVQHCCKLFGWSYGSLSL 180
 QY 181 QMGEADISGYIPNGEWDLVGPGRKSRFRFYECCKEPEYPDVTFTTMRRTLYYGLNLLIP 240
 Db 181 QMGEADISGYIPNGEWDLVGPGRKSRFRFYECCKEPEYPDVTFTTMRRTLYYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTFTMLLVABEIMPATSDSVPLIAQYFAST 300
 Db 241 CVLISALALVFLPADSGEKISLGITVLLSLTFTMLLVABEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVTVIQLYHHDDPGKPKWTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVTVIQLYHHDDPGKPKWTRVILLNWCWFLMRKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGDPDLAKILEEVRYIANRFRCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-08-700-636-8
 ; Sequence 8, Application US/08700636
 ; Patent No. 5910582
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,636
 ; FILING DATE: 16-JUL-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/028,031
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reiter, Stephen E.
 ; REGISTRATION NUMBER: 31,192
 ; REFERENCE/DOCKET NUMBER: P41 9368
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-4737
 ; TELEFAX: 619-546-9392
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 502 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-700-636-8

Query Match 79.9%; Score 401; DB 2; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Db 121 RFDATFHTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 4

US-08-467-574-8
; Sequence 8, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Elliot, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-467-574-8

Query Match 79.9%; Score 401; DB 3; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNVPLRPVANDSQPLTVYFSL 60
Qy 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNTNWLQSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Db 121 RFDATFHTNVLNVSNGHCQYLPFGIKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVTFTVMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPPDVTFTVMRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLIGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLMRKPGEDKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 5

US-09-217-345-8
; Sequence 8, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Elliot, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe
 STREET: 4250 Executive Square, 7th Floor
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/466,589
 FILING DATE: 05-JUN-95
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9949B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-450-8400
 TELEFAX: 619-587-5360
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 502 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-09-217-345-8

Query Match 79.9%; Score 401; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120

QY 121 REDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 REDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180

QY 181 QMEADISGYPNGEWDLVGIPKRSRFEYCKEPEYDVTFTVTMRRTLYYGLNLLIP 240
 DB 181 QMEADISGYPNGEWDLVGIPKRSRFEYCKEPEYDVTFTVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHK 360
 DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHK 360

QY 361 QRCCLASVEMSAVAPPASGNLLYIGFRGLDGVHCVPPTDPSGVGCRMACSTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPASGNLLYIGFRGLDGVHCVPPTDPSGVGCRMACSTHDEHL 420

QY 421 LHGGQPEGPDIAKILEEVRYIANRRCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

DB 421 LHGGQPEGPDIAKILEEVRYIANRRCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
 US-08-487-596-12
 Sequence 12, Application US/08487596
 Patent No. 640681
 GENERAL INFORMATION:
 APPLICANT: Elliot, Kathryn J.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Harpold, Michael M.
 TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
 TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
 TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,596
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO US94/02447
 FILING DATE: 08-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/938,154
 FILING DATE: 30-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/504,455
 FILING DATE: 03-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9951
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 502 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-487-596-12

Query Match 79.9%; Score 401; DB 4; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKYLKVNPNPLRPVANDSOPLTVYFSL 60

QY 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTIWLQMSWTDHYLQWNVSEYPGVKTFRFDCQIWKPDILLYNSADE 120

QY 121 REDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 REDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180

QY 181 QMEADISGYPNGEWDLVGIPKRSRFEYCKEPEYDVTFTVTMRRTLYYGLNLLIP 240
 DB 181 QMEADISGYPNGEWDLVGIPKRSRFEYCKEPEYDVTFTVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHK 360
 DB 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPAQCHK 360

QY 361 QRCCLASVEMSAVAPPASGNLLYIGFRGLDGVHCVPPTDPSGVGCRMACSTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPASGNLLYIGFRGLDGVHCVPPTDPSGVGCRMACSTHDEHL 420

QY 421 LHGGQPEGPDIAKILEEVRYIANRRCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480

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QY 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQNMVSEYGVKTVRPPDGOIWKPDILLYNSADE 120
Db 61 QIMDVDEKNOVLTNNIWLQSWTDHYLQNMVSEYGVKTVRPPDGOIWKPDILLYNSADE 120
QY 121 RFDATHTNNVLSNNSGHCQYLPPGIPKSSCVIVRWPFDFVQHCCKLFGWSYSGWSL 180
Db 121 RFDATHTNNVLSNNSGHCQYLPPGIPKSSCVIVRWPFDFVQHCCKLFGWSYSGWSL 180
QY 181 QMGEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db 181 QMGEADISGYPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVABIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVLQVHHDDPGKMPKWTIRVILLNWCWFLRMKPGEDKVPACQHK 360
Db 301 MIIVGLSVVTVTVLQVHHDDPGKMPKWTIRVILLNWCWFLRMKPGEDKVPACQHK 360
QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDPDLAKILEEVRYIANRFRQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNVEAVSKDFA 502
Db 481 ICTIGILMSAPNVEAVSKDFA 502

```

```

RESULT 7
US-08-278-635B-7
; Sequence 7, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-7
Query Match
Best Local Similarity 12.4%; Score 62; DB 1; Length 502;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
Db 29 LYKELVKYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
QY 89 WN 90
Db 89 WN 90
RESULT 8
US-08-464-258B-7
; Sequence 7, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-258B-7
Query Match
Best Local Similarity 12.4%; Score 62; DB 3; Length 502;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
Db 29 LYKELVKYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTNNIWLQSWTDHYLQ 88
QY 89 WN 90
Db 89 WN 90

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Db 89 WN 90

RESULT 9
US-08-471-961-7
; Sequence 7, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,961
; FILING DATE: 21-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-7

Query Match 12.4%; Score 62; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LYKELVKNYPLRPVANDSQPLTVYFSLQLQIMVDKNOVLTTNIWLQMSWTDHYLQ 88
|||||
Db 29 LYKELVKNYPLRPVANDSQPLTVYFSLQLQIMVDKNOVLTTNIWLQMSWTDHYLQ 88
|||||

QY 89 WN 90
||
Db 89 WN 90

RESULT 10
US-08-278-635B-8
; Sequence 8, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-635B-8

Query Match 5.4%; Score 27; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVFLLPADSGEKISLGITVLLSLT 273
|||||
Db 255 LALLVFLLPADSGEKISLGITVLLSLT 281
|||||

RESULT 11
US-08-464-258B-8
; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:

;; NAME: REITER, STEPHEN E.
;; REGISTRATION NUMBER: 31,192
;; REFERENCE/DOCKET NUMBER: P41 9989
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-677-1409
;; TELEFAX: 619-677-1465
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 511 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-464-258B-8

Query Match 5.4%; Score 27; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVLLPADSGEKISLGTIVLLSLT 273
Db 255 LALLVLLPADSGEKISLGTIVLLSLT 281

RESULT 12
US-08-471-961-8
; Sequence 8, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,961
; FILING DATE: 21-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-8

Query Match 5.4%; Score 27; DB 3; Length 511;
Best Local Similarity 100.0%; Pred. No. 7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVLLPADSGEKISLGTIVLLSLT 273
Db 255 LALLVLLPADSGEKISLGTIVLLSLT 281

RESULT 13
US-08-278-635B-2
; Sequence 2, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-2

Query Match 2.0%; Score 10; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 NLLIPCVLIS 245
Db 243 NLLIPCVLIS 252

RESULT 14
US-08-464-258B-2
; Sequence 2, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-258B-2

Query Match 2.0%; Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 236 NLLIPCVLIS 245
Db 243 NLLIPCVLIS 252
RESULT 15
US-08-471-961-2
Sequence 2, Application US/08471961
Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.

REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-2
Query Match 2.0%; Score 10; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 236 NLLIPCVLIS 245
Db 243 NLLIPCVLIS 252
Search completed: June 20, 2003, 19:15:03
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:52:00 ; Search time 23 Seconds
(without alignments)
905.266 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGVWLALASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2698	99.8	502	1	ACH7_HUMAN
2	2545	94.2	502	1	ACH7_MOUSE
3	2536	93.8	499	1	ACH7_BOVIN
4	2531	93.6	502	1	ACH7_RAT
5	2429	89.9	502	1	ACH7_CHICK
6	1107.5	41.0	498	1	ACH1_CAEEL
7	960.5	35.5	516	1	ACH1_MANSE
8	947	35.0	557	1	ACH1_SCHGR
9	945	35.0	529	1	ACH2_HUMAN
10	940.5	34.8	511	1	ACH2_RAT
11	938.5	34.7	459	1	ACHN_CARAU
12	937.5	34.7	528	1	ACH2_CHICK
13	935.5	34.6	576	1	ACH2_DROME
14	934	34.6	622	1	ACH4_CHICK
15	932	34.5	503	1	ACH3_HUMAN
16	922	34.1	496	1	ACH3_CHICK
17	922	34.1	567	1	ACH1_DROME
18	916	33.9	627	1	ACH4_HUMAN
19	915.5	33.9	495	1	ACH3_BOVIN
20	913	33.8	495	1	ACHP_RAT
21	908	33.6	630	1	ACH4_RAT
22	901.5	33.4	499	1	ACH3_RAT
23	884	32.7	494	1	ACH6_CHICK
24	884	32.7	498	1	ACHP_HUMAN
25	878	32.5	521	1	ACH3_DROME
26	876.5	32.4	491	1	ACHN_CHICK
27	876	32.4	470	1	ACHP_CHICK
28	874	32.3	512	1	ACH3_CARAU
29	867.5	32.1	450	1	ACHX_HUMAN
30	867.5	32.1	494	1	ACH6_HUMAN
31	862.5	31.9	493	1	ACH6_RAT
32	861	31.9	502	1	ACHN_HUMAN
33	857	31.7	457	1	ACHA_RAT

34	852.5	31.5	479	1	ACH9_HUMAN	Q9ugm1 homo sapien
35	850	31.4	457	1	ACHA_MOUSE	P04756 mus musculus
36	849.5	31.4	511	1	ACH5_CAEEL	Q23022 caenorhabdi
37	847	31.3	538	1	ACH8_CAEEL	P45963 caenorhabdi
38	845	31.3	457	1	ACHA_BOVIN	P02709 bos taurus
39	842	31.2	519	1	ACH4_DROME	P25162 drosophila
40	839	31.0	456	1	ACHA_CHICK	P09479 gallus gall
41	837	31.0	500	1	ACHN_RAT	P12390 rattus norv
42	832.5	30.8	479	1	ACH9_RAT	P43144 rattus norv
43	829.5	30.7	456	1	ACHA_BRARE	Q98880 brachydanio
44	829.5	30.7	457	1	ACH1_XENLA	P22456 xenopus lae
45	822.5	30.4	464	1	ACHO_RAT	P12391 rattus norv

ALIGNMENTS

RESULT 1

ACH7_HUMAN STANDARD; PRT; 502 AA.
AC P36544; Q15826; Q99555; Q96RH2; Q9BXH0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR NACHRA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94195283; PubMed=8145738;
RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
from the SH-SY5Y cell line and determination of pharmacological
properties of native receptors and functional alpha 7 homomers
expressed in Xenopus oocytes.";
RT Mol. Pharmacol. 45:546-554(1994).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Hippocampus;
RC Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicellebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
beta 4 subunits.";
RT J. Mol. Neurosci. 7:217-228(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RT FEBS Lett. 400:309-314(1997).
RN [5]
RP REVISIONS.
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidermal keratinocytes;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes.";

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7] SEQUENCE OF 17-502 FROM N.A.
 RP TISSUE=Brain;
 RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human a7 nicotinic acetylcholine
 RT receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 RN [8]
 RP SEQUENCE OF 24-502 FROM N.A.
 RP TISSUE=Retina;
 RX MEDLINE=94245114; PubMed=8188270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human alpha 7-
 RT nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 RN [9]
 RP SEQUENCE OF 118-129 FROM N.A.
 RX PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the alpha7-
 RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 RN [10]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 CC
 CC EMBL; X70297; CAA49778.1; -;
 CC EMBL; U40583; AAB3561.1; -;
 CC EMBL; U62436; AAB4014.1; -;
 CC EMBL; Y08420; CAA69697.1; -;
 CC EMBL; AF385585; AAK6811.1; -;
 CC EMBL; L25827; -; NOT ANNOTATED_CDS.
 CC EMBL; Z23141; CAA80672.1; -;
 CC EMBL; AF332758; AAK19515.1; -;
 CC Genew; HGNC:11960; CHRNA7.
 CC MIM; 118511; -;
 CC InterPro; IPR000188; GABAA receptor.
 CC InterPro; IPR001175; Neur.Chan.Channel.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan_mem; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRFAM; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family.

FT	SIGNAL	1	22	BY SIMILARITY.
FT	CHAIN	23	502	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT				ALPHA-7 CHAIN.
FT	DOMAIN	23	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	255	POTENTIAL.
FT	TRANSMEM	262	280	POTENTIAL.
FT	TRANSMEM	296	317	POTENTIAL.
FT	DOMAIN	318	469	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	470	490	POTENTIAL.
FT	DISULFID	150	164	BY SIMILARITY.
FT	DISULFID	212	213	ASSOCIATED WITH RECEPTOR ACTIVATION
FT				(BY SIMILARITY).
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	11	11	A -> G (IN REF. 1 AND 7).
FT	CONFLICT	58	58	S -> N (IN REF. 2 AND 6).
FT	CONFLICT	134	134	S -> P (IN REF. 2 AND 6).
FT	CONFLICT	364	364	C -> S (IN REF. 8).
FT	CONFLICT	375	375	A -> G (IN REF. 1).
FT	CONFLICT	409	413	RMACS -> AWPAP (IN REF. 8).
FT	SEQUENCE	502 AA;	56449 MW;	D94B3A482EAA0E42 CRC64;
QY				Query Match 99.8%; Score 2698; DB 1; Length 502;
DB				Best Local Similarity 99.8%; Pred. No. 2.3e-213;
QY				Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB				1 MRCSPGGVWLAALASLHVSLQGEFQRLKYLKYNVNPRLPVPANDSQPLTVVFSLSLL 60
QY				1 MRCSPGGVWLAALASLHVSLQGEFQRLKYLKYNVNPRLPVPANDSQPLTVVFSLSLL 60
DB				61 QIMDVDEKNOVLTNINWQSWTDHYLQWNVSEYPGVKTVPDQGWKPDILLYNSADE 120
QY				61 QIMDVDEKNOVLTNINWQSWTDHYLQWNVSEYPGVKTVPDQGWKPDILLYNSADE 120
DB				121 RFDAFTNTNVLNSSGHCCQYLPFGIFKSSCYIDVRWFFPDVQHCKLFGSGWSYGLDL 180
QY				121 RFDAFTNTNVLNSSGHCCQYLPFGIFKSSCYIDVRWFFPDVQHCKLFGSGWSYGLDL 180
DB				181 QMOEADISGYIPNGEWDLVIPGKRSEFYECCKEYPDVTFTVTRRTLYYGLNLLIP 240
QY				181 QMOEADISGYIPNGEWDLVIPGKRSEFYECCKEYPDVTFTVTRRTLYYGLNLLIP 240
DB				241 CVLISALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDVPLIAQYFAS 300
QY				241 CVLISALALLVFLPADSGEKISIGITVLLSLTFMLLVAEIMPATSDVPLIAQYFAS 300
DB				301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWRVILLNWCANFLMRKPGEDKVRPACQHK 360
QY				301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWRVILLNWCANFLMRKPGEDKVRPACQHK 360
DB				361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDBHL 420
QY				361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDBHL 420
DB				421 LHGGQPPGDDPLAKILEEYVIANRRCQDESEAVCSEWFAACVVDRLCLMAPSVFTI 480
QY				421 LHGGQPPGDDPLAKILEEYVIANRRCQDESEAVCSEWFAACVVDRLCLMAPSVFTI 480
DB				481 ICTIGILMSAPNFVEAVSKDFA 502
QY				481 ICTIGILMSAPNFVEAVSKDFA 502
DB				481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2
 ACH7 MOUSE
 ID -ACH7_MOUSE STANDARD; PRT; 502 AA.
 AC P49582;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACRA7.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95324936; PubMed=7601470;
RA Orr-Urtreger A., Seidlin M.F., Baldini A., Beaudet A.L.;
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
RL acetylcholine receptor."
RL Genomics 26:399-402(1995).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L37663; AAC2053.1; --
DR MGD; MGI:99779; Chrna7.
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT
FT DOMAIN 23 230 ALPHA-7 CHAIN.
FT TRANSMEM 231 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 262 280 POTENTIAL.
FT TRANSMEM 296 317 POTENTIAL.
FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DISULFID 150 164 BY SIMILARITY.
FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
FT
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;

Query Match 94.2%; Score 2545; DB 1; Length 502;
Best Local Similarity 93.8%; Pred. No. 7.6e-201;
Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGVMLAALASHVSIQGFQRLKYELKYNVPLRPVANDSQPLTVYFSLQLQIMDV 65
DB 6 GGVMLAALASHVSIQGFQRLKYELKYNVPLRPVANDSQPLTVYFSLQLQIMDV 65

QY 66 DEKNQVLTINILQMSWTBHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADERFDT 125
DB 66 DEKNQVLTINILQMSWTBHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADERFDT 125

QY 126 FHTNVLNNSGHCQYLPFGIKSSCYIDVRWPFDPVQHCCLKFGSGSYGWSLDLQMOEA 185
DB 126 FHTNVLNNSGHCQYLPFGIKSSCYIDVRWPFDPVQHCCLKFGSGSYGWSLDLQMOEA 185

QY 186 DISGYIPNGEWDLVGIPKRSRFRFYECCKEPPDVTFTVTRRRRTLYYGLNLLIPCVLIS 245
DB 186 DISSYIPNGEWDLMGIPGRNEKFYECCKEPPDVTFTVTRRRRTLYYGLNLLIPCVLIS 245

QY 246 ALALLVFLLPADSGEKISLIGITVLLSLTTEMLLVAEIMPATSDSVPPLTAQYFASWTMIIVG 305
DB 246 ALALLVFLLPADSGEKISLIGITVLLSLTTEMLLVAEIMPATSDSVPPLTAQYFASWTMIIVG 305

QY 306 LSVVVTVIVLOYHHRHDPDGGKMPKTRVILLNWCWFLRMKRPDGDVKRPAQCHKORRCS 365
DB 306 LSVVVTVIVLRVYHHRHDPDGGKMPKTRVILLNWCWFLRMKRPDGDVKRPAQCHKORRCS 365

QY 366 LASVEMSAVAPPPASNGMLLYIFGRGLDVHCVPTPDGSGVCGRMACSPTHDEHLHGGQ 425
DB 366 LASVELSAGAGPPTSGNLLYIFGRGLEGMHCAPTDPDGSVCGRLACSPTHDEHLHMGTH 425

QY 426 PEGDPPDLAKLILEEVRYIANRFRCODESEAVCESEKFAACVVDRLCLMAFSPFTICTIG 485
DB 426 PSDGPPDLAKLILEEVRYIANRFRCODESEVCESEKFAACVVDRLCLMAFSPFTICTIG 485

QY 486 ILSAPNFEAVSKDFA 502
DB 486 ILSAPNFEAVSKDFA 502

RESULT 3
ACH7_BOVIN STANDARD; PRT; 499 AA.
ID ACH7_BOVIN STANDARD; PRT; 499 AA.
AC PS4131;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=95346009; PubMed=7620615;
RA Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
RA Gutierrez L., Criado M.;
RT "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine
RT chromaffin cells: molecular cloning, functional expression and
RT alternative splicing of the alpha 7 subunit."
RL Eur. J. Neurosci. 7:647-655(1995).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO
CC UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT
CC FORMS OF THE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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DR EMBL; X93604; CAAC3802.1; --
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 499
FT
FT DOMAIN 20 227
FT TRANSMEM 28 252
FT TRANSMEM 259 277
FT TRANSMEM 293 314
FT DOMAIN 315 466
FT TRANSMEM 467 487
FT DISULFID 147 161
FT DISULFID 209 210
FT
FT CARBOHYD 43 43
FT CARBOHYD 87 87
FT CARBOHYD 130 130
FT VARSPLIC 262 290
SQ SEQUENCE 499 AA; 56002 MW; ABE5D0B3820D42D5 CRC64;
Query Match 93.8%; Score 2536; DB 1; Length 499;
Best Local Similarity 94.4%; Pred. No. 4.1e-200;
Matches 469; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
QY 6 GGWTLAASLLHVSLOGEFORLYKELVKNYNPLRPVANDSOPLYFSLSLQIMDV 65
Db 3 GSICLAASILHVSLOGEFORLYKDLVKNYNPLRPVANDSOPLYFSLSLQIMDV 62
QY 66 DEKNQVLTNIWQMSWTDHYLWNVSEYPGVKTVPDGOIWKPDILLYNSADERFDT 125
Db 63 DEKNQVLTNIWQMTWTDHYLWNVSEYPGVKTVPDGOIWKPDILLYNSADERFDT 122
QY 126 FHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPFDVQVCKLKFGWSYSGWSLQMQEA 185
Db 123 FHTNVLVNSGHCQYLPPIGFKSSCYIDVRWFPFDVQVCKLKFGWSYSGWSLQMQEA 182
QY 186 DISGYIPNGEWDLVGLPGKSEKRYECCKEPYDPVTFTVWRRRTLYGLNLLPCVLIS 245
Db 183 DISGYIPNGEWDLVGLPGKSEKRYECCKEPYDPVTFTVWRRRTLYGLNLLPCVLIS 242
QY 246 ALALLVFLPADSGEKISLGLTVLLSLTTTMLVAEIMPATSDSVPLIAQYFASMTIIVG 305
Db 243 ALALLVFLPADSGEKISLGLTVLLSLTVFLLVAEIMPATSDSVPLIAQYFASMTIIVG 302
QY 306 LSVVTVIVLQYHHDDPGGKMPKWTQVILNWCWFLRMKRPGEKVRPACQHKQRCS 365
Db 303 LSVVTVIVLQYHHDDPGGKMPKWTQVILNWCWFLRMKRPGEKVRPACQHKQRCS 362
QY 366 LASVMSAVAPPASNNLYIGRGLDGVHCVPTDPSGVVCGVMACSPTHDEHLLHGQ 425
Db 363 LASVMSAVAGPATNGNLLYIGRGLDGVHCVPTDPSGVVCGVMACSPTHDEHLLHAGQ 422
QY 426 PPSGDDPLAKTLEVRVYIANFRFCODESEAVCESEKFAACVVDRLCLMAFVFTICTIG 485
Db 423 PPSGDDPLAKTLEVRVYIANFRFCODESEAVCESEKFAACVVDRLCLMAFVFTICTIG 482
QY 486 ILSAPNFVEAVSKDFA 502
Db 483 ILSAPNFVEAVSKDFA 499
RESULT 4
ACH7 RAT
ID ACH7 RAT
AC Q05941;
STANDARD; PRT; 502 AA.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=931147931; PubMed=7678857;
RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
RT "Molecular cloning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
calcium.";
RL J. Neurosci. 13:596-604(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Boulter J.;
RX Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISION TO 363.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Hartley M.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S53987; AAB25224.2; --
CC EMBL; L31619; AAC33136.1; --
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
DR Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502
FT
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT
FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT CONFLICT 447 447
N -> F (IN REF. 2).

FT CONFLICT 469 469 P -> R (IN REF. 2).
SQ SEQUENCE 502 AA; 56410 MW; 00996574EC7B9A56 CRC64;

Query Match 93.6%; Score 2531; DB 1; Length 502;
Best Local Similarity 93.4%; Pred. No. 1.1e-199;
Matches 464; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 6 GGWLALAAALLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
DB 6 GGWLALAAALLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVYFSLSLQIMDV 65
QY 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIWKPDILLYNSADERFDAT 125
DB 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVRPDGOIWKPDILLYNSADERFDAT 125
QY 126 FHTNVLVNSGHCHQYLPPIGFKSSCYIDVRWFPDVOHQCKLKFGSWSYGSLSLQMQEA 185
DB 126 FHTNVLVNSGHCHQYLPPIGFKSSCYIDVRWFPDVOHQCKLKFGSWSYGSLSLQMQEA 185
QY 186 DISGYIPNGEWDLVGIPKRSERFYECKEPPYDVTFTVWRRRTLYGLNLLIPCVLIS 245
DB 186 DISGYIPNGEWDLVGIPKRSERFYECKEPPYDVTFTVWRRRTLYGLNLLIPCVLIS 245
QY 246 ALALLVFLPADSGEKISLIGITVLLSTTFLMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
DB 246 ALALLVFLPADSGEKISLIGITVLLSTTFLMLVAEIMPATSDSVPLIAQYFASTMIIVG 305
QY 306 LSVVVTVIVLQYHHHPDGGKMPKTRVILLNWCWFLRMKRPGECKVVRACQKQRCS 365
DB 306 LSVVVTVIVLQYHHHPDGGKMPKTRVILLNWCWFLRMKRPGECKVVRACQKQRCS 365
QY 366 LASVENSAVAPPASNGNLLYIGFRGLDGVHCVTPDSDGVVCGRMACSPTHDEHLRHGGQ 425
DB 366 LASVELSAGAPPTSGNLLYIGFRGLEGMHCAPTDPDSDGVVCGRLACSPTHDEHLMHGAH 425
QY 426 PEGDPLAKILEEYRIANRFRQDESEAVCEWKEAACVVDRLCLMAFSVFTIITIG 485
DB 426 PSDGDPDLAKILEEYRIANRNRQDESEVICSEWKEAACVVDPLCLMAFSVFTIITIG 485
QY 486 ILMSAPNFVEAVSKDFA 502
DB 486 ILMSAPNFVEAVSKDFA 502

RESULT 5
ACH7 CHICK
ID ACH7 CHICK STANDARD; PRT; 502 AA.
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
RA Millar N., Valera S., Barks T., Ballivet M.;
RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
RT developmentally regulated and forms a homo-oligomeric channel blocked
RT by alpha-BTX.";
RL Neuron 5:847-856(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstroem J.;
RT "Brain alpha-bungarotoxin binding protein cDNAs and MADS reveal

subtypes of this branch of the ligand-gated ion channel gene
superfamily.";
RL Neuron 5:35-48(1990).
RN [3]
RP SEQUENCE OF 1-18 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzinski L., Hernandez M.C., Rostocil T., Ballivet M.,
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
RT promoter develops during morphogenesis of the central nervous
RL system.";
RL EMBO J. 11:4529-4538(1992).
RN [4]
RP SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
RA Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but
RT homologous proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN [5]
RP MUTAGENESIS OF LEU-270.
RX MEDLINE=92049732; PubMed=1719423;
RA Hecuh F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic.";
RL Nature 359:500-505(1992).
RN [6]
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829;
RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic.";
RL Nature 359:500-505(1992).
RN [7]
RP FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -! SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
SIMILARITY).
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
CC -! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
CC EMBL; X52295; CAA36543.1; -;
CC EMBL; X68246; CAA48317.1; -;
CC EMBL; X68586; CAA48576.1; -;
CC PIR; JN0113; JN0113.
CC PIR; B25738; B25738.
CC PIR; JH0172; JH0172.
CC InterPro; IPR000188; GABAA receptor.
CC InterPro; IPR001175; Neur channel.
CC Pfam; PF02931; Neur_chan_IID; 1.
CC Pfam; PF02932; Neur_chan_Memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
CC Postsynaptic membrane; Glycoprotein; Signal;
CC Transmembrane; Multigene family.
KW

```
FT SIGNAL 1 23
FT CHAIN 24 502
FT FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT FT ALPHA-7 CHAIN.
FT FT EXTRACELLULAR.
FT DOMAIN 24 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT FT CARBOHYD 46 46
FT CARBOHYD 90 90
FT CARBOHYD 133 133
FT MUTAGEN 270 270
FT FT CONFLICT 26 27
FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
SQ
Query Match 89.9%; Score 2429; DB 1; Length 502;
Best Local Similarity 90.7%; Pred. No. 2.4e-191;
Matches 449; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
Qy 8 VWLALASLHVSLOGEFQRLKYLKYNLPNPLRPVANDSQPLTVYFSLSLQIMDVDE 67
Db 8 LWLALAAGLVRESLOGEFQRLKYLKYNLPNPLRPVANDSQPLTVYFSLSLQIMDVDE 67
Qy 68 KNOVLTTNWLQSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNADERFDATFH 127
Db 68 KNOVLTTNWLQSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNADERFDATFH 127
Qy 128 TNLVNSSGHCOYLPPGIFKSSCYIDVRWPFDPVOHCKLKFGSWSYGGWSLDLQMOEADI 187
Db 128 TNLVNSSGHCOYLPPGIFKSSCYIDVRWPFDPVOHCKLKFGSWSYGGWSLDLQMOEADI 187
Qy 188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISAL 247
Db 188 SGYISNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISAL 247
Qy 248 ALLVFLPADSGEKISIGITVLLSLTFMFLVAEIMPATSDSVPLIAQYFASPMIIVGLS 307
Db 248 ALLVFLPADSGEKISIGITVLLSLTFMFLVAEIMPATSDSVPLIAQYFASPMIIVGLS 307
Qy 308 VVTVTVLVQYHHDDPGCKPKTRVILLNKCWFLMKRPGEDKVRPACQHKORCSLA 367
Db 308 VVTVTVLVQYHHDDPGCKPKTRVILLNKCWFLMKRPGEDKVRPACQHKORCSLS 367
Qy 368 SVMSAVAPPPASNGNLLYIGFRGLDGVCHVPTPDGVCVGRMACSPTHDBHLHGGOPP 427
Db 368 SMENVTSGQCCSNGNMLYIGFRGLDGVCHVCTPTDSDGVCIGRWTCSPTEENLHSGHPS 427
Qy 428 EGGPDLAKILEEVRYIANRRFCQDESAVCSEMKFAACVVDRLCLMAFVSFTIICIGIL 487
Db 428 EGGPDLAKILEEVRYIANRRFRQDEEAEICNEWFAFASVVDRLCLMAFVSFTIICIGIL 487
Qy 488 MSAPNFVEAVSKDFA 502
Db 488 MSAPNFVEAVSKDFA 502
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RESULT 6

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ACH1_CABEL STANDARD; PRT; 498 AA.
ID ACH1_CABEL
AC P48180;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor like protein, alpha-type chain precursor.
GN F25G6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
```

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OK NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=96196478; PubMed=8627624;
RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.";
RL J. Mol. Biol. 258:261-269 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohldmann P.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; X83887; CAA58764.1; --
CC EMBL; AF022973; AAC25796.1; --
CC HSP; P58154; 119B.
CC WormPep; F25G6.3; CE09639.
CC InterPro; IPR001188; GABAA receptor.
CC InterPro; IPR001175; Neur. Channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_mem; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane; signal.
FT SIGNAL 19
FT CHAIN 20 498
FT FT POTENTIAL.
FT FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
FT FT ALPHA-TYPE CHAIN.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT TRANSMEM 231 252
FT TRANSMEM 261 279
FT TRANSMEM 295 314
FT DOMAIN 315 472
FT TRANSMEM 473 493
FT DISULFID 147 161
FT DISULFID 211 212
FT FT ASSOCIATED WITH RECEPTOR ACTIVATION
FT FT (BY SIMILARITY).
FT FT CARBOHYD 43 43
FT CARBOHYD 93 93
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;
Query Match 41.0%; Score 1107.5; DB 1; Length 498;
Best Local Similarity 44.6%; Pred. No. 3.8e-83;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;
Qy 10 LALAASLHVSLOGEFO-RKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMDVDEK 68
Db 6 LLISCAILAAPTLGSLOERRLYEDLMRNYNPLRPVANDSQPLTVYFSLSLQIMDVDEK 65
Qy 69 NOVLTTNWLQSWTDHYLQWNVSEYGVKTVRPPDQGIWKPDILLYNADERFDATFH 128
Db 66 NOVVVNAWLDYTWNDYLVNDKAEYGNITDVRFPAGKIWKPDILLYNADERFDATFH 125
Qy 129 NVLVNSSGHCOYLPPGIFKSSCYIDVRWPFDPVOHCKLKFGSWSYGGWSLDLQMOEAA--D 186
Db 126 NMIVYSTGLVHWVPPGIFKISKIDIQWFFPEQKCFKFSWTVYDGYKLDLQPATGGFD 185
Qy 187 ISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTMRRRTLYYGLNLLIPCVLISA 246
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Db 186 ISEYISNGEWALPLTTVERNEKFYDCPEYDPVHFLHMRRTLYYGFNLMPICILFTL 245
 QY 247 LALLVFLPADSEKISLGITVLLSLTFLMLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 Db 246 MTLGLFTLPDAGEKITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFTCCMIVVTA 305
 QY 307 SVVTVTVLVQVHHDPGGKMKWKTRVILLNWCFAFLRMKRPBGDKVRPACQKQRCSL 366
 Db 306 STVTVTVLVNLHRTPTDHMGPTWRNLLLVWIPWILRMKRPG-----HNLTVASL 356
 QY 367 ASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDS-----GVVCGRMAC 412
 Db 357 PSL-----FSTKPNRHSLSLRNIK--DNEHSLSRANSFADACRLNQYIMTQSVSNGLTSL 410
 QY 413 SPTHDEHLHGQPPGEGDP-----LAKILEEVYIANRFRQDESEAVCSWEKFAACV 467
 Db 411 GSIPSTMISSNGTTTVDVSOQATLLHLRIYHELKIIVTKRMTEGDKKEQACNWKFAAMV 470
 QY 468 DRCLMAFVSFTICTIGILMSAPNFV 494
 Db 471 DRCLVFTTIIIVSTIGIFWSPALV 497

RESULT 7

ACH1 MANSE
 ID ACH1 MANSE STANDARD; PRT; 516 AA.
 AC P91766;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain precursor (MARA1).
 GN ARA1.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 OC Ditrysia; Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98424077; PubMed=9753155;
 RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
 RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
 RT "Characterization of a nicotinic acetylcholine receptor from the
 insect Manduca sexta."
 RL Eur. J. Neurosci. 10:879-889(1998).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y09795; CAA70928.1; -
 DR InterPro; IPR000188; GABAA Receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 516 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 FT LIKE CHAIN.

FT DOMAIN 22 243
 FT TRANSMEM 244 264
 FT TRANSMEM 274 294
 FT TRANSMEM 306 326
 FT DOMAIN 327 465
 FT TRANSMEM 466 486
 FT DISULFID 149 163
 FT DISULFID 222 223
 FT CARBOHYD 45 45
 FT CARBOHYD 132 132
 FT CARBOHYD 233 233
 SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13BD2 CRC64;
 Query Match 35.5%; Score 960.5; DB 1; Length 516;
 Best Local Similarity 40.4%; Pred. No. 4.3e-71;
 Matches 196; Conservative 88; Mismatches 166; Indels 35; Gaps 6;
 QY 27 RLYKELVKNYPLRPPVANDSOPLTVYFSLQIMDVDEKNQVLTNIWLMQSWTDHY 86
 Db 26 KRLYDDLSSNYKLRVPLVNSDALTVRIKLSQLIDVNLKQIMTNLWTEQSWDYK 85
 QY 87 LQNVSEYPGVKTRFPDQIWKPDILLYNSADERFDATEHTNVLVNSSGHCOYLPPIG 146
 Db 86 LSWEPREYGGVEMLHVPSDHIWRPDVLYNNADGNFVTLATKATNTTGRVEMRPPAIY 145
 QY 147 KSSCYIDVRWFPFDVQHCKLFGSNGSLDQMQE-----ADISGYIPNGE 195
 Db 146 KSSCEIDVEYFPDQTCVMKFGSWTYDGFQDLRHRIDEVGRGTNNVVELGVDSLEYTSVE 205
 QY 196 WDLVGIPOKRSERYECCKEPYDVTFTVWRRRTLYYGLNLLIPCVLISALALLVFLP 255
 Db 206 WDILEVPAVRNEKFYTCDEPYLDITFNITRRKTLFTVNLIIIPCMGISFLTLLVFLP 265
 QY 256 ADSGEKISLGTLLSLTTFMLLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVVVL 315
 Db 266 SDSGEKVSLISISILLIIFLLIABIIPTTSLVVLGKFLFTMTLDTFSICVTVVVL 325
 QY 316 QYHHHDPDGGKMPKTRVILLNWCFAFLRMKRPBGDKVRPACQKQRCSLASVMSAVA 375
 Db 326 NVHFRSQTHMSPWVRVFIHVLPRLLVMRPP-HYRLDP---HRSRAGLV----- 374
 QY 376 PPPASNGNLLYIGFRGLDGVHCVTPDPSGVVVCGR-----MACSPTHDEHLHGQPPGD 430
 Db 375 --GAGETTLWDEGSPG-----VPAPRPPPCAPPELAPCAACAPAEALCDALRRWHRC 426
 QY 431 PDLAKILEEVYIANRFRQDESEAVCSWEKFAACVDRCLMAFVSFTICTIGILMSA 490
 Db 427 PELHKAIDGINYIADQTRKEEESTRVKEDWKYVAMVLDPRPFLWITFLAVVVGSAIILQA 486
 QY 491 PNFVE 495
 Db 487 PTLVD 491

RESULT 8

ACH1 SCHGR
 ID ACH1 SCHGR STANDARD; PRT; 557 AA.
 AC P23414;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha-L1 chain precursor.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
 OC Schistocerca
 OX NCBI_TaxID=7010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91092263; PubMed=1702381;
 RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,

RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RL insect nicotinic acetylcholine receptor.";
EMBO J. 9:4391-4398 (1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X55439; CAA39081.1; -;
CC PIR; S12359; S12359.
CC InterPro; IPR000188; GABAA receptor.
CC InterPro; IPR001175; Neur_chan channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFS; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT DOMAIN 24 244 EXTRACELLULAR.
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT CARBOHYD 47 47
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 382 400 ALA/SER-RICH.
FT DOMAIN 406 422 HIS-RICH.
FT SEQUENCE 557 AA; 63026 MW; 168389C887DFDF3E CRC64;

Query Match 35.0%; Score 947; DB 1; Length 557;
Best Local Similarity 37.1%; Pred. No. 6.1e-70;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGCVLALASLLHVSILQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMD 64
DB 6 PPMALLLLHHPAAANPAKLYDDLSNLYNRLRPVSNNTDTVLKVLGLRLSOLID 65

QY 65 VDERKQVLTNIWLMQSWTHYLOWNVSEPGVKTVPDPDQIQKPDILLNSADRPDA 124
DB 66 LNLKQDQITTNVLEHEWQDHKFRWDPAEYGVTELYVPSEHIMLPDVLVYNADGEYV 125

QY 125 TPTHTNLVNSGHCQYLPPIGFKSSCYIDVRWFPDQVQCKLFGSWSYGCWSDLDQ--- 181
DB 126 TWTAKVLLHTGKVVWTPPAIFKSCSDIDRVYFFPDQTCFMKFGSWTYDGDIDLKHIN 185

QY 182 -----MOEADISGYPNGEWDLVIGPKRSERFVCECKEYPDVTFVTMRRTLYY 233
DB 186 QKYDDNKVKVIGIDLREYVPSVENDILGPAERHEKYPPCCAEYPDIFNITLRKTLFY 245

QY 234 GLNLLPCVLISALALVFLPADSGKISIGITVLLSLTFTFMLLVAEIMPATSDSVPLI 293
DB 246 TVNLIVPCVGSYLSVLVFLPADSGEKALICISILLSTQTMFFLLISIPSTSLALPLL 305

QY 294 AQYFASTMIIVGLSVVTVIVLYQHHHPDQGGKMPKTRVILLNWCAMFLMRKPRGE--- 350

RESULT 9
ACH2_HUMAN STANDARD; PRT; 529 AA.
ID AC01-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Hypothalamus;
RX MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RT J. Mol. Neurosci. 7:217-228(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Groot Kormelink P.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Blechschmidt K., Rosenthal A.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC
CC EMBL; U62431; AAB40109.1; -;
CC EMBL; Y16281; CAA76154.1; -;
CC EMBL; AF311103; -; NOT_ANNOTATED_CDS.

P12389; O08952;
01-OCT-1989 (Rel. 12, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
CHRNA2 OR ACR2.
Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
RN "Functional expression of a new pharmacological subtype of brain
nicotinic acetylcholine receptor.";
RL Science 240:330-334(1988).
[2]
RN REVISIONS.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RC Boulter J.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC
CC EMBL; LI0077; AAB60900.1; -
CC EMBL; M20297; AAA40664.1; -
CC EMBL; M20292; AAA40664.1; JOINED.
CC EMBL; M20293; AAA40664.1; JOINED.
CC EMBL; M20294; AAA40664.1; JOINED.
CC EMBL; M20295; AAA40664.1; JOINED.
CC EMBL; M20296; AAA40664.1; JOINED.
CC InterPro; IPR000188; GABAA receptor.
CC Dfam; PF02931; Neur_chan_IbD; 1.
CC Dfam; PF02932; Neur_chan memb; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
CC Postsynaptic membrane, ionic channel; Glycoprotein; Signal;
CC Transmembrane; Multigene family.
CC SIGNAL 1 27 POTENTIAL.
CC FT CHAIN 28 511 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
CC FT EXTRACELLULAR.
CC FT DOMAIN 28 241 POTENTIAL.
CC FT TRANSMEM 242 266 POTENTIAL.
CC FT TRANSMEM 274 232 POTENTIAL.
CC FT TRANSMEM 308 329 POTENTIAL.
CC FT DOMAIN 330 484 CYTOPLASMIC.
CC FT TRANSMEM 485 503 POTENTIAL.
CC FT DOMAIN 391 402 POLY-GLU.
CC FT DISULFID 160 174 BY SIMILARITY.
CC FT DISULFID 224 225 ASSOCIATED WITH RECEPTOR ACTIVATION
CC (BY SIMILARITY).
CC FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT


```

FT CARBOHYD 212 212 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 494 494 C -> S (IN REF. 1; AAA40664).
SQ SEQUENCE 511 AA; 58611 MW; 3824E83BB01D613B CRC64;

Query Match
Best Local Similarity 34.8%; Score 940.5; DB 1; Length 511;
Matches 201; Conservative 82; Mismatches 180; Indels 53; Gaps 9;

QY 8 VW--LALASLLHVSLOGSFQRLKYLKYNPLERPVANDSOPLTVYFSLQLQMDV 65
DB 16 LNCILLVPAVLTOQSGHTAEDELFLKHLFGYNRWPVNTSDVIVRGLSIAQLIDV 75

QY 66 DEKNQVLTNNIQLQMSWTDHYLQWNVSEYPGVKTVPDQIQWKPDILLYNSADERDAT 125
DB 76 DEKNQVMTNNVQLKQWMDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGRAVT 135

QY 126 FHTNVLVNSGHCQYLPPIGIFKSCSVIDVWFFDVQHCCLKGWSYGGWSLDLQMOE- 184
DB 136 HMTKAHLFTGTGVHWVPPALYKSSCSIDVTFPPDQCNCKWFGSWTYDKAKIDLEQMER 195

QY 185 -ADISGYIPNGEWDLVGIPGKRSERFVECKEYVDVTFVTWRRRLTYGLNLLIPCVL 243
DB 196 TVDLKDYWESGEWAIINATGYNKSYDCCAEYDPDVTYFVIRRLPLFTINLIIPCLL 255

QY 244 ISALALLVFLPADSGEKISGLITVLISLFTFMMLVAEIMPATSDSVPLIAQVFASTMI 303
DB 256 ISCLTVLVYFLPSECKEKITCLISVLLSLTVFLLITELIIPSTSLVPLICEYLLFTMIF 315

QY 304 VGLSVVTVVIVLYQHHPDGGKMPKWRVILLNWCAMFLRMKRP-----GDKVRPA 356
DB 316 VTLSIVITVFLNVHRSSTHNNPNWVRVALLGRVPRWLMNRPPLPMELHSGPDLKLS 375

QY 357 COHKQRCSLASVEMSAVAPPASNGNLLYIGRGLDGVHCVPPTDS--GVVCGRMACSP 414
DB 376 PSYHLETNMDAGERETEBEEDENICV-----CAGLPDSMGVLYG----- 420

QY 415 THDEHLHGG-----OPPEG-----DPDLAKILEBRYIANRFRQDESEAVCS 458
DB 421 -----HGLHLRAMEPEKTPSQASEILLSQIQKALEGVHYIADRLSEADSSVKE 473

QY 459 EWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
DB 474 DNKYAMVVDRIELWFLIIVCFGLTGIGLF--PPFL 507

RESULT 11
ACHN_CARAU STANDARD; PRT; 459 AA.
AC P19370;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, beta-2 chain (GF-beta-2) (Fragment).
DE Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OC NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=90384858; PubMed=2402468;
RA Hieber V.C., Bouche J.E., Agranoff B.W., Goldman D.;
RT "Nucleotide and deduced amino acid sequence of the goldfish neural
RT nicotinic acetylcholine receptor beta-2 subunit.";
RL Nucleic Acids Res. 18:5307-5307(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
```

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X54052; CAA37986.1; -.
CC PIR; S14703; S14703.
CC InterPro; IPR000188; GABAA receptor.
CC InterPro; IPR001175; Neur Channel.
CC Pfam; PF02931; Neur_chan_LBD; 1.
CC Pfam; PF02932; Neur_chan_memb; 1.
CC TIGRFAMs; TIGR00860; LIC; 1.
CC PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
CC Transmembrane; Multigene family.
CC NON_TER 1 1
CC DOMAIN <1 203 EXTRACELLULAR.
CC TRANSMEM 204 228
CC TRANSMEM 236 254
CC TRANSMEM 270 291
CC DOMAIN 292 421
CC TRANSMEM 422 440
CC CARBOHYD 21 21 N-LINKED (GLCNAC... ) (POTENTIAL).
CC DISULFID 125 139 BY SIMILARITY.
CC CARBOHYD 138 138 N-LINKED (GLCNAC... ) (PROBABLE).
CC SEQUENCE 459 AA; 53040 MW; 860B1A011AA47CF6 CRC64;

Query Match 34.7%; Score 938.5; DB 1; Length 459;
Best Local Similarity 38.5%; Pred. No. 2.4e-69;
Matches 189; Conservative 95; Mismatches 142; Indels 65; Gaps 8;

QY 35 KYNPLRPVANDSOPLTVYFSLQLQMDVDEKNOVLTNNIQLQMSWTDHYLQWNVSEY 94
DB 10 ERYNKLIRPAVNSQQVTIGIKVSLAQILSVNERQIMTNVLTQETDRLWDPNEY 69

QY 95 PGKTVTRFPDQIQWKPDILLYNSADERDATFHTNVLVNSGHCQYLPPIGIFKSCSIDV 154
DB 70 EGIKKLRIPOSHIWLDPDIVLYNNADGVYEVSYFYNVAVNTGDIPLWLPALYKSACATEV 129

QY 155 RWFPFDVQHCCLKFGWSYGGWSLDLQMOE--ADISGYIPNGEWDLVGIPKRSRFFVEC 212
DB 130 RNFPFDQCNCTLKFRSWTYDRTDELVLTSDFASRDDYTPSGEWDIVSLPGRKNE----- 184

QY 213 CKEP-----YPDVTFVTMRRTLYGLNLLIPCVLISALALLVFLPADSGEKISGLITV 268
DB 185 --DNNDLTLDITYDFVKKRPLFTINLIIPCVLITSLAILVFLPSDCGEKVTLCMSV 242

QY 269 LLSLTFMLVAEIMPATSDSVPLIAQVFASTMIIVGLSVVTVVIVLQVHHHPDGGKMP 328
DB 243 LLALTVELLSKIVPPTSLAVPLIGKLMFTWLVTSIVTSVCVNLVHRSPTHTMP 302

QY 329 KWRVILLNWCAMFLRMKRPGEDEVKVRPAQCHQKQRCSLASVEMSAVAPPASNGNLLYIG 388
DB 303 EWKCVFLHLKLPALFLMRPGRSNVRFRFRKQRKSPSSHQ----- 344

QY 389 FRGLDGVHCVPPTSDSGVCGRMACSPHDEHLLHGGQPEG-----DPDLAKIL 437
DB 345 ----DGDSFFLTDDPGRVCGAWRV-----GDLPEGSEFRQVRKVRHQDQVDEAI 389

QY 438 EEVRYIANRFRQDESEAVCEWKFACVDRCLCMAPSVFTIICTIGILMSAPNF---- 493
DB 390 DGVRFIAEHMKIEDDEGIIEDWKVAVMIDRLFWIFILVCVGTGLGLFVQ-PLFQSN 448

QY 494 ---VEAVSKOF 501
DB 449 TPVAEEVYGF 459
```

RESULT 12	ACH2	CHICK	STANDARD;	PRT;	528 AA.
AC	P09480;				
DT	01-MAR-1989	(Rel. 10, Created)			
DT	01-MAR-1989	(Rel. 10, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-2 chain precursor.				
DE	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OC	NCBI_TaxID=9031;				
RN	[1]				
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Brain;				
RC	MEDLINE=88281624; PubMed=3267226;				
RX	Nef P., Oneyser C., Allod C., Couturier S., Ballivet M.;				
RA	"Genes expressed in the brain define three distinct neuronal				
RT	nicotinic acetylcholine receptors.";				
RL	EMBO J. 7:595-601(1988).				
CC	-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN				
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND				
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA				
CC	MEMBRANE.				
CC	-1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT				
CC	TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A				
CC	FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND				
CC	THREE NON-ALPHA CHAINS.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.				
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CC	or send an email to license@isb-sib.ch).				
DR	ENBL; X07339; CAB59645.1; -				
DR	ENBL; X07340; CAB59645.1; JOINED.				
DR	ENBL; X07341; CAB59645.1; JOINED.				
DR	ENBL; X07342; CAB59645.1; JOINED.				
DR	ENBL; X07343; CAB59645.1; JOINED.				
DR	ENBL; X07344; CAB59645.1; JOINED.				
DR	ENBL; AJ250360; CAB59625.1; -				
DR	PIR; S03377; ACCH2N.				
DR	InterPro; IPR000188; GABAA receptor.				
DR	InterPro; IPR001175; Neur_Channel.				
DR	Pfam; PF02931; Neur_chan_I BD; 1.				
DR	Pfam; PF02932; Neur_chan_mem; 1.				
DR	PRINTS; PR00252; NRIONCHANNEL.				
DR	TIGRFAMS; TIGR00860; LIC; 1.				
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.				
KW	Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;				
KW	Transmembrane; Multigene family.				
FT	SIGNAL	1			
FT	CHAIN	24 528			
FT	DOMAIN	24 239			
FT	TRANSMEM	240 264			
FT	TRANSMEM	272 290			
FT	TRANSMEM	306 327			
FT	DOMAIN	328 501			
FT	TRANSMEM	502 520			
FT	DOMAIN	394 410			
FT	DISULFID	158 172			
FT	DISULFID	222 223			
FT	CARBOHYD	54 54			
FT	CARBOHYD	104 104			

RL FEBS Lett. 269:264-268(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90360975; PubMed=1697262;
 RA Sawruk E., Schloss P., Betz H., Schmitt B.;
 RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
 RL EMBO J. 9:2671-2677(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolehakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherly J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulo G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkaskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS
 CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC AND LATE PUPAL STAGES.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X52274; CAA36517.1; --
 CC EMBL; X53583; CAA37652.1; --
 CC EMBL; AE003748; AAF56303.1; --
 CC PIR; S11679; ACFFA2.
 CC FlyBase; FBgn0000039; nAChR-alpha-96Ab.
 CC InterPro; IPR000188; GABAA_receptor.

DR InterPro; IPR001175; Neur channel.
 DR Pfam; PF02931; Neur chan_LBD; 1.
 DR Pfam; PF02932; Neur chan memb; 1.
 DR PRINTS; TR00252; NRIONCHANNEL.
 DR TIGRFAMs; TRG00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 21 PROBABLE.
 FT CHAIN 22 576 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
 FT DOMAIN 22 261 LIKE CHAIN 2. (POTENTIAL).
 FT TRANSMEM 262 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 311 POTENTIAL.
 FT TRANSMEM 327 346 POTENTIAL.
 FT DOMAIN 347 526 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 527 545 POTENTIAL.
 FT DISULFID 169 183 BY SIMILARITY.
 FT DISULFID 243 244 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT CARBOHYD 65 65 (BY SIMILARITY).
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 576 AA; 6506 MW; 97D6A46CAD3F42F CRC64;
 Query Match 34.6%; Score 935.5; DB 1; Length 576;
 Best Local Similarity 38.1%; Pred No. 5.5e-69;
 Matches 203; Conservative 102; Mismatches 185; Indels 43; Gaps 9;
 Qy 3 CSPGVWLAASLLHVSLOGE-FQRLYKELVKNYNPLERPVANDSOLTVYFSLSLQ 61
 Db 23 CKP--LCLLVLLLCETVQANPAKRLDYLDDLLSYNNRLIRPVSNNTDTVLKGLRLSQ 80
 Qy 62 IMDVDKQVLTNNIWLQMSWDHYLQWVSEYGVKTVRFPDQGIWKPDIILYNSADER 121
 Db 81 LIDLNLKQILTTNWLEHEWQDHFKFWDPEYGVGVTELYVPSEHILWLPDVLVYNADGE 140
 Qy 122 FDATEHTNVLNSSGHCOYLPFGFKSSCYIDVWFEPDVOHCKLFGSWSVGGWSDL- 180
 Db 141 YVVTMTKAILHYTGKVVVTPPAIFKSSCEIDVRYFPDQOTCFMKFGSWYDGGQIDLK 200
 Qy 181 ---QMGE-----ADISGYIPNGEWDLVGIPGRSERFYECCKEYPDVTFTVMRRR 229
 Db 201 HISQNDKDNKVEIGIDREYVPSVENDILGVPAERHEKYYPCCAEPYDIFNITLRK 260
 Qy 230 TLYYGLNLLIPCVLISALALIVFLPADSGSKISLGITVLVLSLTFTMLLVAEIMPATSDS 289
 Db 261 TLFYTNLLIPCVGISVLSVLVFLPADSGEKIALCISILLSQTMFFLLISEIIPSTSLA 320
 Qy 290 VPLIAQYFASPMIIVGLSVVTVVIVLYQVHHHPDGGKMPKWTVRVILLNWCANFLMKRPG 349
 Db 321 LPLLGKYLFTMLLVGLSVVITIIILNIHYRKPSTHKRMPWIRSFIFKRLPKLLLMRVP- 379
 Qy 350 EDKVRPACQKHOR-----RCSLASVEMSAVAPPASPNGLL-YIGRGLDGVHC 397
 Db 380 KDLRLDLANKINYLKFSKTKFGQALMDENQMSGSSPSLRMQRGVAGGCGMHV 439
 Qy 398 VPTPD--SGVV-----CGRMACSPTHDEHLLHGGQPPGPDPAKILEEVRY 442
 Db 440 TTATNRFSGLVGALGGGLSTLSGYNGLPSVLSGLDSDLSVAAARKKYPFELEKATHVMF 499
 Qy 443 IANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTICTIGILMSAPNFE 495
 Db 500 IQHEMQRQDEFAEDQDMGFVAMVMDRLFLWLFMIASLVGTGTVILGEAPSLYD 552
 RESULT 14
 ACH4 CHICK
 ID ACH4 CHICK STANDARD; PRT; 622 AA.
 AC P09482;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE	Neuronal acetylcholine receptor protein, alpha-4 chain precursor.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX	Gallus.
RN	NCBI_TaxID=9031;
[1]	
RN	SEQUENCE FROM N.A.
RP	TISSUE=Brain;
RC	MEDLINE=88283624; PubMed=3267226;
RA	Nef P., Oneysver C., Alliod C., Couturier S., Ballivet M.;
RT	"Genes expressed in the brain define three distinct neuronal
RL	nicotinic acetylcholine receptors.";
RN	EMBO J. 7:595-601(1988).
[2]	
RN	MUTAGENESIS OF GLU-289, AND SUBUNITS.
RP	MEDLINE=91172320; PubMed=2005979;
RA	Cooper E., Couturier S., Ballivet M.;
RT	"Pentameric structure and subunit stoichiometry of a neuronal
RL	nicotinic acetylcholine receptor.";
RN	Nature 350:235-238(1991).
CC -I-	FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC	EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC	MEMBRANE.
CC	-I- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC	TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC	FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC	THREE NON-ALPHA CHAINS.
CC -I-	SUBCELLULAR LOCATION: Integral membrane protein.
CC -I-	SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC	
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CC	or send an email to license@lsb-sib.ch).
CC	
DR	ENBL; X07348; CAA30285.1; --
DR	ENBL; X07349; CAA30285.1; JOINED.
DR	ENBL; X07350; CAA30285.1; JOINED.
DR	ENBL; X07351; CAA30285.1; JOINED.
DR	ENBL; X07352; CAA30285.1; JOINED.
DR	ENBL; X07353; CAA30285.1; JOINED.
DR	ENBL; X07399; CAA30285.1; JOINED.
DR	ENBL; AJ250361; CAB59626.1; --
DR	PIR; S00379; ACCH4N.
DR	InterPro; IPRO00188; GABAA receptor.
DR	InterPro; IPRO01175; Neur Channel.
DR	Pfam; PF02931; Neur_chan_LBD; 1.
DR	Pfam; PF02932; Neur_chan_mem; 1.
DR	PRINTS; PR00252; NRIONCHANNEL.
DR	TIGRFAMS; TIGR00860; LIC; 1.
DR	POSTSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW	Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW	Transmembrane; Multigene family.
FT FT	SIGNAL
FT FT	CHAIN 1 223
FT FT	DOMAIN 24 622
FT FT	TRANSFAM 24 237
FT FT	TRANSMEM 238 262
FT FT	TRANSFAM 270 288
FT FT	TRANSMEM 304 325
FT FT	DOMAIN 326 595
FT FT	TRANSMEM 596 614
FT FT	DISULFID 156 170
FT FT	DISULFID 220 221
FT FT	CARBOHYD 52 52
FT FT	CARBOHYD 102 102
FT FT	MUTAGEN 289 289
FT FT	
FT FT	BY SIMILARITY.
FT FT	(BY SIMILARITY)
FT FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT	E->K; REDUCES CHANNEL CONDUCTANCE BY
FT FT	HALF.

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OM protein - protein search, using sw model

Run on: June 20, 2003, 18:56:36 ; Search time 44 Seconds
(without alignments)
1096.806 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGGWIALAALLHVS.....TIGILMSAPNFVEAVSKDFA 502
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2690	99.5	502	1	ACHUA7
2	2690	99.5	502	2	G02259
3	2545	94.2	502	2	A57175
4	2531	93.6	502	2	T01378
5	2429	89.9	502	2	JN0113
6	1816.5	67.2	511	2	JH0173
7	1107.5	41.0	498	2	S68588
8	1089.5	40.3	560	2	T19822
9	998	36.9	461	2	T25671
10	947	35.0	557	2	S12359
11	944	34.9	542	2	T19862
12	942.5	34.9	511	2	A40110
13	938.5	34.7	459	2	S14703
14	937.5	34.7	528	1	ACCH2N
15	936.5	34.6	503	2	A53956
16	935.5	34.6	576	1	ACFPA2
17	934	34.6	622	1	ACCH4N
18	933	34.5	502	2	A37040
19	922	34.1	567	1	ACFPA1
20	916	33.9	627	2	JC4021
21	915.5	33.9	495	2	S60589
22	913.5	33.8	625	2	A26456
23	912	33.7	495	2	B35721
24	898	33.2	494	2	T09289
25	895	33.1	517	2	A30992
26	887.5	32.8	499	2	A24572
27	884	32.7	498	2	G02421
28	877	32.4	521	1	ACPFNN
29	876.5	32.4	491	1	ACCHNN

30	876	32.4	470	2	A39218	nicotinic acetylch
31	874	32.3	512	2	B37014	nicotinic acetylch
32	861	31.9	502	2	S10505	nicotinic acetylch
33	857	31.7	457	2	S13872	nicotinic acetylch
34	850	31.4	457	2	A24383	nicotinic acetylch
35	849.5	31.4	511	2	T43634	nicotinic acetylch
36	848	31.4	445	2	I49458	acetylcholine rece
37	845	31.3	457	1	ACBOA1	nicotinic acetylch
38	844.5	31.2	500	2	S12899	nicotinic acetylch
39	842	31.2	457	1	ACHUA1	nicotinic acetylch
40	839	31.0	456	1	ACCHAN	nicotinic acetylch
41	838.5	31.0	503	2	JH0174	nicotinic acetylch
42	837.5	31.0	468	2	T24724	hypothetical prote
43	832.5	30.8	479	2	A53382	nicotinic acetylch
44	829.5	30.7	457	2	S08162	nicotinic acetylch
45	828	30.6	474	2	T27006	hypothetical prote

ALIGNMENTS

RESULT 1

ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain

C:Species: Homo sapiens (man)

C>Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999

C:Accession: I37185; A54194; S60309

R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the omers expressed in Xenopus oocytes.

A:Reference number: I37185; MUID:94195283; PMID:8145738

A:Accession: I37185

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-502 <PEN>

A:CROSS-references: EMBL:X70297; NID:G496606; PIDN:CAA49778.1; PID:G496607

A:Experimental source: brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzarotti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic A:Reference number: A54194; MUID:94245214; PMID:8188270

A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:CROSS-references: GB:Z23141; NID:G457736; PIDN:CAA80672.1; PID:G457737

A:Experimental source: retina

C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized C:Genetics:

A:Gene: GDB:CHRNA7

A:CROSS-references: GDB:I38751; OMIM:118511

A:Map position: 15q14-15q14

A:Note: defects in this gene have been associated with mental retardation and schizophrenia C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains a

C:Superfamily: acetylcholine receptor

C:Keywords: brain; Glycoprotein; heteropentamer; ion channel; neurotransmitter receptor

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred

F:231-254/Domain: transmembrane #status predicted <TR1>

F:262-280/Domain: transmembrane #status predicted <TR2>

F:296-317/Domain: transmembrane #status predicted <TR3>

F:470-488/Domain: transmembrane #status predicted <TR4>

F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Disulfide bonds: #status predicted

F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

Best Local Similarity 99.5%; Score 2690; DB 1; Length 502;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADE 120
 QY 121 RFDPATFTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
 DB 121 RFDPATFTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPEGDDPAKILEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPEGDDPAKILEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Molecule type: mRNA
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 99.5%; Score 2690; DB 2; Length 502;
 Best Local Similarity 99.4%; Pred. No. 3.4e-221;
 Matches 499; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADE 120
 DB 61 QIMDVDEKNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADE 120
 QY 121 RFDPATFTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
 DB 121 RFDPATFTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 180
 QY 181 QMGEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 240
 DB 181 QMGEADISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGCKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRCCLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPEGDDPAKILEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPEGDDPAKILEEVRYIANRFRQDESEAVSEWKFACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 94.2%; Score 2545; DB 2; Length 502;
 Best Local Similarity 93.8%; Pred. No. 7.8e-209;
 Matches 466; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 6 GGWMLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 65
 DB 6 GGWMLAALASLLHVSLOGEFQRLKYLKLVKNYNPLERPVANDSQPLTVYFSL 65
 QY 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADERF 125
 DB 66 DEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDILLYNSADERF 125
 QY 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 185
 DB 126 FHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDDVQHCCKLFGSWSYGGWSL 185
 QY 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 245
 DB 186 DISGYIPNGEWDLVGIPGKRSERFYECCKEYPYDVTFTVTMRRTLYYGLNLLIP 245
 QY 246 ALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 305
 DB 246 ALALVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 305

Db 128 TNVLNSSGHCOYLPPIGFKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 187
QY 188 SGVINGEWDLVGIPIKRSERFVECCKEPYDPVDTFTVWRRRTLYYGLNLLIPCVLISAL 247
Db 188 SGVINGEWDLVGIPIKRSERFVECCKEPYDPVDTFTVWRRRTLYYGLNLLIPCVLISAL 247
QY 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
Db 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
QY 308 VVTVIVLYOYHHDDPGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSLA 367
Db 308 VVTVIVLYOYHHDDPGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSLA 367
QY 368 SVEMSAVAPPASNGNLLYIGFGLDGVCHVCTPDSGVCGMACSPTHDEHLLHGQPP 427
Db 368 SVEMSAVAPPASNGNLLYIGFGLDGVCHVCTPDSGVCGMACSPTHDEHLLHGQPP 427
QY 428 EGDPDLAKILEEVRYIANRPRCODESEAVCESEKFAACVVDRLCLMAFVSFTIICIGIL 487
Db 428 EGDPDLAKILEEVRYIANRPRCODESEAVCESEKFAACVVDRLCLMAFVSFTIICIGIL 487
QY 488 MSAPNFVEAVSKDFA 502
Db 488 MSAPNFVEAVSKDFA 502

RESULT 6
JH0173
A:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
A:Experimental source: brain
A:Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.2%; Score 1816.5; DB 2; Length 511;
Best Local Similarity 68.8%; Pred. No. 9.5e-147;
Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
QY 8 VMLAASLLHVSLOGEFORKLYKELVKNYNPLERPANDSQPLTVYFSLQLQIMDVDE 67
Db 16 LWASLFLSPFKVQOQGESQRLDLRNYNLERPWNDSQPIVBLQLSLQIIDVE 75
QY 68 KNQVLTNIWQMSWDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADERFDATFH 127
Db 76 KNQVLTNIWQMSWDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADERFDATFH 135
QY 128 TNVLNSSGHCOYLPPIGFKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 187
Db 136 TNVLNVSQCOYIPPGILKSTCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEADI 195
QY 188 SGVINGEWDLVGIPIKRSERFVECCKEPYDPVDTFTVWRRRTLYYGLNLLIPCVLISAL 247

Db 196 SNYISNGEWDLVGPGRKNELYYECCKEPYDPVDTFTVWRRRTLYYGLNLLIPCVLISGL 255
QY 248 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 307
Db 256 ALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLS 315
QY 308 VVTVIVLYOYHHDDPGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHK--QRRK 364
Db 316 VVTVIVLYOYHHDDPGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHK--QRRK 374
QY 365 SLASVENSAPPASNGNLLYIGFGLDGVCHVCTPDSGVCGMACSPTHDEHLLHG 424
Db 375 SLKNTENMVLPHQPSNGNMIY-SYHTMENPCCPQNDLGSKGKICTCLPSEDEMEHVQKK 433
QY 425 QPEGDPDLAKILEEVRYIANRPRCODESEAVCESEKFAACVVDRLCLMAFVSFTIIC 484
Db 434 ALMDTIVIVKILEVOFIAMRFKQDEGEIASEWFAAAVDRCLVLAFTLPAICTF 493
QY 485 GILMSAPNFVEAVSKDF 501
Db 494 TILMSAPNFVEAVSKDF 510

RESULT 7

S68588
A:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT

Query Match 41.0%; Score 1107.5; DB 2; Length 498;
Best Local Similarity 44.6%; Pred. No. 2.4e-86;
Matches 226; Conservative 77; Mismatches 167; Indels 37; Gaps 7;
QY 10 LALAASLLHVSLOGEFORKLYKELVKNYNPLERPANDSQPLTVYFSLQLQIMDVDEK 68
Db 6 LLISCAILLAAPTLGSLOERRLYDLMRNYNLERPVANHSPEVTVHLKVALQIIDVDEK 65
QY 69 NQVLTNIWQMSWDHYLQWNVSEYPGVKTVRFPDQGIWKPDILLYNSADERFDATFH 128
Db 66 NQVTVVNAWLDYTWNDYNLVMDKAEYGNITDVRFPAGIKWPDVLLYNSVDTFDSTYQT 125
QY 129 NVLVNSSGHCOYLPPIGFKSSCYIDVRWPFDFVQKCNLKFSGSWTYCGNSLDLQMOEA--D 186
Db 126 NMIVYSTGLVHWVPPGIFKISCKIDIOFPPEDEQKCFKFGSWTYDGYKLDQPATGFD 185
QY 187 ISGYIPNGEWDLVGIPIKRSERFVECCKEPYDPVDTFTVWRRRTLYYGLNLLIPCVLISA 246
Db 186 ISEYISNGEWALPLTTVERNEKFYDCCPEPYDVHFLHMRRTLYYGFNLMPCILITL 245
QY 247 LALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306
Db 246 MTLGFTLPPDAGEKITLQITVLLSICFSLSVSEMSPTSEAVPLLGIFFTCCMIVVTA 305
QY 307 SVVTVIVLYOYHHDDPGGKMPKWRVILLNWCWFLRMKRPBGDKVRPACQHKQRCSL 366
Db 306 STVFVTVVNLHYRTPTHDMGMPWTRNLLLYWIMILMRKRPG-----HNLTYASL 356
QY 367 ASVEMSAVAPPASNGNLLYIGFGLDGVCHVCTPDS-----GVVCGRMAC 412

Db 357 PSL-----FSTKPNRHSLSIRNIK--DNEHSLSRANSFADCRNLNQYIMTQSVNSGLTSL 410
Qy 413 SPFHDEHLLHGGQPPGDPD-----LAKILEEYVYIANRFRQDESEAVCSWEKFAACVW 467
Db 411 GSIPSTMISSNGTTTDSVQOATLILHRIYHELVKIVTKRMTEGDKKEQACNNKWKFAAMV 470
Qy 468 DRCLMAFVSFTTICTIGILMSAPNV 494
Db 471 DRCLVYFTFIIVSTIGIFWSAPYLV 497

RESULT 8
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07843.1; GSPDB:GN00019; CESP:C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 40.3%; Score 1089.5; DB 2; Length 560;
Best Local Similarity 40.6%; Pred. No. 9.5e-85;
Matches 226; Conservative 93; Mismatches 157; Indels 81; Gaps 9;

Qy 10 LALAASLL-----HVSLOGERQKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQI 62
Db 8 LVLVSILIWETKCSKVITWGDHERRLYAKLAENYNKLARPVNRESEAVVLLGMDYQOI 67
Qy 63 MDVDERNOVLTITNIMQMSWTDHYLOWNVSEYGVKTVRPDGOIWKPDILLYNSADERF 122
Db 68 LDIDEXHQIMNSVNLWMSWTDHYLTWDPSEFGNKEVRLPINNWKPDVLLYNSVDPQOF 127
Qy 123 DATFTFNVLNVSCHQYLPPIGFKSCYIDVWFFPDVQHCCLKFGSWSYGSLSLQ 182
Db 128 DSTWPNVAVLYTGNVTWIPALIRSCAIDIAFPDTHCTWKFSGWTSYGFDTLIN 187
Qy 183 QEADISGYIPNGEWDLVGIPGKRSERFYECCKPEYDPDVTFTVMRRRTLYYGLNLLIPCV 242
Db 188 TTISATYKPNGEWELLGLTSQRSIFFEYECPEPYDVTFTVSIRRTLYYGFNLLPCM 247
Qy 243 LISALALLVFLPADSGEKISLIGITVLLSLTTMFLVAEIMPATSDSVPLIAQYFASTMI 302
Db 248 LISSALLSFTLPADCGEKLNGVTIFMSLCVFMIWVAEMPQTSALPLIQIFYSCIMF 307
Qy 303 IYGLSVVTVIVLYQHHHDPDGK-MPKWTRVILLNWCAMFLMKRPGEDKVRPACOH-- 359
Db 308 QVGSVAIVIAVLFNHRHSPQYKPNKFKLTKLLGLLPTLLGMRPDVLELSVHGAYHA 367
Qy 360 ----KORRCSLASVEMSAVAPPASNGNLLYIGFRGLD----- 393
Db 368 SDNKKQRYLLEVERHILTRP---NGN-----GHSADVAKVHLDLSTGNPHSDAKSSPS 420
Qy 394 -----GVHCVPFP-----DSGV---VCGRMACSPHDBHLHGGQPPGDPD----- 431
Db 421 PKRTSASIMGMTCLPTTMQNGALDSSINKYCTKVTPLNGSATINHKSPPINPINN 480
Qy 432 -----DLAKILEEYVYIANRFRQDESEAVCSWEKFAACVDRCLCLMAF 475
Db 481 NTKCANNOKTQFEDRHHFHLNELRVISARVKEEAMHALQADWMPFASRVDRVCFLAF 540
Qy 476 SVFTTICTIGILMSAPN 492

Db 541 SAFLPMCTAISYNAPH 557

RESULT 9
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 36.9%; Score 998; DB 2; Length 461;
Best Local Similarity 39.8%; Pred. No. 4.6e-77;
Matches 197; Conservative 96; Mismatches 146; Indels 56; Gaps 8;

Qy 12 LAASLLHVSL--QGEF--QRKLYKELVKNYNPLRPVANDSQPLTVYFSLSLQIMVDENK 69
Db 10 LSLVIIHSNLCDSVAETKLTDLKLYGNPLRPVQNSSQPLEVKIKLFLQQLIDVDENK 69
Qy 70 QVLTNTNQLQMSWTDHYLOWNVSEYGVKTVRP--DQIWKPDILLYNSADERDAPFH 127
Db 70 QIVSNWALSYTWDHKLQWEPKYGIGIQDIRFGSSDHIWKPDVLLYNSAAEDFDSTFK 129
Qy 128 TNVLVNSGHQYLPPIGFKSCYIDVWFFPDVQHCCLKFGSWSYGSLSLQ 182
Db 130 SNLTYHTGTWVTPPGVLKVCQLDVTWFFPDQVCEMKFGSWTFHGYAIDLQIDDDTN 189
Qy 183 --QEADISGYIPNGEWDLVGIPGKRSERFYECCKPEYDPDVTFTVMRRRTLYYGLNLLIP 240
Db 190 GTQSMDLSTLVNGEWQVISTNAKRVSYKKCCPEYPTVNYLHRRRTLYYGFNLLIP 249
Qy 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTMFLVAEIMPATSDSVPLIAQYFAST 300
Db 250 SLLISLMAILGFMFPDAGEKITLEVITLLAIVFSLMSVSEMTPTSEAVPLIGVFFSCC 309
Qy 301 MIIVGLSVVTVIVLYQHHHDPDGKMPKWKTRVILLNWCAMFLMKRPGEDKVRPACQHK 360
Db 310 MLVVSASVFTIVVNLNLFHSADSHENMPLVRRVLLLEFLPMLFMSRPGYKFKV-- 363
Qy 361 --QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCV--TPDSGVVCGRMACSPHDBH 419
Db 364 -----ANV-----IDSTDMKPKPKPLDNLPSNHAGYEAQ 395
Qy 420 LLHGGQPPGDPDLAKILEEYVYIANRFRQDESEAVCSWEKFAACVVDRLCLMAFVSFT 479
Db 396 ILL-----LHSVHTELRRVVAFYFNKEEHERIQTDWRFAAMVVDRACLLLFTVFI 445
Qy 480 ICTIGILMSAPNV 494
Db 446 VISILAIMSAPHII 460

RESULT 10
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359

R;Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.; EMBO J. 9, 4391-4398, 1990
A;Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor
A;Reference number: S12359; MUID:91092263; PMID:1702381
A;Accession: S12359
A;Molecule type: mRNA
A;Residues: 1-557 <MAR>
A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
F;245-266/Domain: transmembrane #status predicted <TM1>
F;274-295/Domain: transmembrane #status predicted <TM2>
F;308-329/Domain: transmembrane #status predicted <TM3>
F;501-523/Domain: transmembrane #status predicted <TM4>
F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 947; DB 2; Length 557;
Best Local Similarity 37.1%; Pred. No. 1.3e-72;
Matches 201; Conservative 92; Mismatches 177; Indels 72; Gaps 6;

QY 5 PGGWIALAASLLHVSLOGEFQRLKYLKVNTPNLPBPVANDSQPLTVFSLSLQIMD 64
DB 6 PMLLLLLLLHHPAAANPDARLYDLSNRYLRIPVSNNTDTVLVXGLRLSLQID 65
QY 65 VDEKNOVLTNINWQSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADERFDA 124
DB 66 LNKQQLITNINWLEHWDHQRWDPAEYGGVTELYVPSEHILWPDIVLNNADGYYV 125
QY 125 THTNVLNVSNGHCOYLPPGIFKSSCYIDVVRFPFDVQHCKLFGSWSYGGWSLDQ--- 181
DB 126 TMTKAVLHHTGKVVWTPPAIFKSSCEIDVRYPPFDQTCFMKFGSWTYDGDQIDLKHIN 185
QY 182 -----MQEADISGYPNGEWDLVGIPGKRSEFYECKEKPYPDVTFTVMRRRLYY 233
DB 186 QKYDDNKVKVIGIDIREYYPSEVWDILGVAERHEKYYPCCAEPYDIFNITLRKTLFY 245
QY 234 GLNLLIPCVLISALALLVFLPADSGEKISIGITVLLSLTFTMLLVAEIMPATSDSVPLI 293
DB 246 TVNLIVPCVGSISLVFLPADSGEKIALCISILLSQTMFFLLSEIIPSTSLAFLPL 305
QY 294 AQYFASTMIIVGLSVVTVIVLQVHHHPDGGKMPKTRVILLNWCWFLRMKPEGE--- 350
DB 306 GKYLFTWLVGLSVITIVLVNHYKPKSTKMAVWVKVIRRLPKLLMRVPEQLLA 365
QY 351 DKVRPAQKHQRCSLASVEMSAVAPPASNGNLLYTGFRGLDGVCHVCPVPDPSGVVCGRM 410
DB 366 DLASKRLRLRAHNSKLSAAAAAATAAASSS-----AASSPDS--LRHHH 408
QY 411 ACSPTHDEHL-LHGGQPEG----- 429
DB 409 LHQHQHQLHLQLHLPQPGCNGLHSATNRPFGSAGAFGGLPSVVGLDGSLDVATRKY 468
QY 430 DPDLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIGILMS 489
DB 469 PFELEKAIHNVLFIONHMQRQDEDAEDQDQMGFVAMVDDRLFLWIFTIASIVGTFAILCE 528
QY 490 AP 491
DB 529 AP 530

RESULT 11
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19862
R;Hemby, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19862

A;Status: preliminary; translated from GB/EMBL/DDDB
A;Molecule type: DNA
A;Residues: 1-542 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A;Experimental source: clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.2
A;Map position: X
A;Inserts: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 464/1;
C;Superfamily: acetylcholine receptor

Query Match 34.9%; Score 944; DB 2; Length 542;
Best Local Similarity 37.7%; Pred. No. 2.3e-72;
Matches 207; Conservative 93; Mismatches 165; Indels 84; Gaps 15;

QY 11 ALAASLLHV-----SLOGEFQRLKYLKVNTPNLPBPVANDSQPLTVFSLSLQIMDV 65
DB 12 ALHCVLFHLLTEVHSSADEY--RLADLRHNDYPERPVANASEPLVSVKYYLQQLIDV 69
QY 66 DEKNOVLTNINWQSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADERFD 123
DB 70 DEKNOVLTNINWQSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADERFD 129
QY 124 ATHTNVLNVSNGHCOYLPPGIFKSSCYIDVVRFPFDVQHCKLFGSWSYGGWSLDQ--- 182
DB 130 STYPNVVSVYTGVDVLPVPGIILKSCIKIDITYFPDDQICHLKFGSWTYSGNFIDLRIN 189
QY 183 -----QEADISGYPNGEWDLVGIPGKRSEFYECKEKPYPDVTFTVMRRRLYY 233
DB 190 GPEGKNTSDEGIDVOYVQNGEWLLAVPARHETNIFD--EOPYPSLFFYLIHQRTLYY 247
QY 234 GLNLLIPCVLISALALLVFLPADSGEKISIGITVLLSLTFTMLLVAEIMPATSDSVPLI 293
DB 248 GLNLLIPCVLISALALLVFLPADSGEKISIGITVLLSLTFTMLLVAEIMPATSDSVPLI 307
QY 294 -----AQYFASTMIIVGLSVVTVIVLQVHHHPDGGKMPKTRVILLNWCWFLRMK 347
DB 308 GLIIFSGAFFSCCLLVSVSVVTVLVNLRNRPETHMSPFLRELLILWLPMLLMRR 367
QY 348 PGEKVRPAQKHQRCSLASVEMSAVAPPASNGNLLYIG-FRGLDGVCHVCPVPDPSG--- 404
DB 368 PG--KTFNCTHLKAEKAEKAKOGSI-----KNG-----VGPGRPTDSVH---PSEGLS 412
QY 405 ----VVCGR-MACSPTHDEHLHGG-----QPEGDP----- 431
DB 413 LMKNIKLRQOTIDFEYEFHVOHMLMPVASEMTPRTVYSKVAESVEDVVMTELNY 472
QY 432 -----DLAKILEEVRYIANFRQDESEAVCSWKFAACVVDRLCLMAFSVFTIICIG 485
DB 473 MQKACLELKNISSQTRAMRKKEEDEDEQAANDKFAAMVVDRCCLITFSFVIVSTCG 532
QY 486 ILMGAPNV 494
DB 533 IMFSSPHLI 541

RESULT 12
A40110
nicotinic acetylcholine receptor alpha-2 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 20-Aug-1999
C;Accession: A40110
R;Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson,
Science 240, 330-334, 1988
A;Title: Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor
A;Reference number: A40110; MUID:88178113; PMID:2832952
A;Accession: A40110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-511 <WAD>
A;Cross-references: GB:M20297; NID:g202672; PIDN:AAA40664.1; PID:g202674
A;Note: the authors translated the codon TCG for residue 494 as Cys
C;Superfamily: acetylcholine receptor

C;Keywords: neurotransmitter receptor

Query Match 34.9%; Score 942.5; DB 2; Length 511;
 Best Local Similarity 39.0%; Pred. No. 2.8e-72;
 Matches 201; Conservative 83; Mismatches 179; Indels 53; Gaps 9;

QY 8 VW-LALAAALLHVSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDV 65
 DB 16 LWCLLVPAVLTOGSHTHAEDRLFKHLFGYINWARPVPNTSDVIVRFLSLAQILDV 75
 QY 66 DEKNQVLTNNIWLQMSQTHYLVQWVSEYPGVKTVPDPGQIWKPKDILLYNASDERFAD 125
 DB 76 DEKNQMTNNVWLKQWENDYKLRWDPAEFGNVTSLRVPSEMINIPDIVLYNADGEFAVT 135
 QY 126 FHTNVLNNSGHCQYLPPIGIFKSCYIDVRWPPDVQHCCLKFGWSYSGWSLDLQWQE- 184
 DB 136 HMTKAHLFFGTGVHVVPPALYKSSCIDVTFPPDQCNCKMFGSWTYDKAKIDLEQWER 195
 QY 185 -ADISGYIPNGEWDLVGIPGKRSERFYECCKEPPYDVTFVTMRRTLYGLNLLIPCVL 243
 DB 196 TVDLKDYWESGEWAIINATYNSKKYDCCAEIYPDVTFYFVIRRLPLFYTNILIPCLL 255
 QY 244 ISALALLFLPLPADSGEKISLIGITVLSLTFMLLVAEIMPATSDSVPLIAQYFASMTII 303
 DB 256 ISCLTVLVFLPSECEKITCLISVLSLTFVLLITELIPSTSLVPLICEYLLFTMIF 315
 QY 304 VGLSVVTVIVLQYHHDDPGGKMPKRWTRVILLNWCWAFRLMKRP-----GEDKVRPA 356
 DB 316 VTLSIVTVFVLNVHRSPTSHNPNWVRVALLGRVPRWLMNRPPLPMELHSGPDLKLS 375
 QY 357 CQHKQRCSLASVEMSAVAPPASNGNLLYIGRGLDGVCHVCPPTDS--GVVCGRMACSP 414
 DB 376 PSYHWTETMDAGERETEETEBEEDENICV-----CAGLPDSSMGVLYG----- 420
 QY 415 THDEHLLHGG-----QPPEG-----DPLAKILEVRYIANRFRQDSEAVCS 458
 DB 421 -----HGGLHURAMEPETKPSQASEILLSPQIQKALEGVHYADRLSEADASSVKE 473
 QY 459 EWKFAACVDRCLCMAFSVFTICTIGILMSAPNFV 494
 DB 474 DMKYVAVWVDRIFLWLFIVISFGTIGLFL--PPFL 507

RESULT 13
 S14703
 Nicotinic acetylcholine receptor beta-2 chain - goldfish (fragment)
 C;Species: Carassius auratus (goldfish)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999
 C;Accession: S14703
 R;Hieber, V.; Bouchey, J.; Agranoff, B.W.; Goldman, D.
 Nucleic Acids Res. 18, 5307, 1990
 A;Title: Nucleotide and deduced amino acid sequence of the goldfish neural nicotinic acetylcholine receptor
 A;Reference number: S14703; MUID:90384858; PMID:2402468
 A;Accession: S14703
 A;Molecule type: mRNA
 A;Residues: 1-459 <HIE>
 A;Cross-references: EMBL:X54052; NID:G62576; PIDN:CAA37986.1; PID:G833601
 C;Superfamily: acetylcholine receptor
 C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;

Query Match 34.7%; Score 938.5; DB 2; Length 459;
 Best Local Similarity 38.5%; Pred. No. 5.4e-72;
 Matches 189; Conservative 95; Mismatches 142; Indels 65; Gaps 8;

QY 35 KYNPLERPVANDSQPLTVYFSLSLQIMDVDEKNQVLTNNIWLQMSQTHYLVQWVSEY 94
 DB 10 ERYNKLIRPAVNKSQOVTIGIKVSLAQSLISVNEREQIMTNVWLTSQWTDYRLWDPNEY 69
 QY 95 PGVKTVPDPGQIWKPKDILLYNASDERFADTFHTNVLNNSGHCQYLPPIGIFKSSCIDV 154
 DB 70 EGIGKLRIPSQHILWLDIYLYNADGVYFVSFCYNAVSNSTGIFWLPPLPAIYKSACAIY 129
 QY 155 RWFPDQVQHCCLKFGWSYSGWSLDLQWQE--ADISGYIPNGEWDLVGIPGKRSERFYEC 212

DB 130 RNFPDQNCVTLKFRSWTYDRTDLVLTSPASRDDYTPSGEWDIVSLPGRKNE----- 184
 QY 213 CKEP-----YPDVTFVTWRRRTLYYGLNLLIPCVLISALALVFLPADSGEKISLIGITV 268
 DB 185 --DPNDLTLDITVDYVIKRPFLFYTNILIPCVLITSLAILVFLPSDCGEKVLCMV 242
 QY 269 LLSLTTFMLVAEIMPATSDSVPLIAQYFASMTIIIVGLSVVTVIVLQYHHDDPGGKMP 328
 DB 243 LLALTVFLLSKIVPPTSLAVPLIKYLMFTWLVTFISIVTSVCLVNVHRSPTTHYMP 302
 QY 329 KWTVILLNWCWAFRLMKRPCEGDKVRPACQHKQRCSLASVEMSAVAPPASNGNLLYIG 388
 DB 303 EWWKCVFLHUKUPAFLLMRPRGRSNVRFRFRHQRKSPSSHQ----- 344
 QY 389 FRGLDGVHCVTPDPSGVVCGRMACSPTHDEHLLHGGQPPEG-----DPLAKIL 437
 DB 345 ---DGDSFFLTDPRVCGAWRV-----GDLPEGSEFQRVKVRHDQVDDEAI 389
 QY 438 BEVRYIANRFRQDSEAVCEWKFACVDRCLCMAFSVFTICTIGILMSAPNF----- 493
 DB 390 DGVRFAIAEHMKIEDDEGIIEDWKYVAMVIDRLFLWIFILVCVGTGLGVQ-PLFQSYN 448
 QY 494 ---VEAVSKDF 501
 DB 449 TPVAEEVYGDF 459

RESULT 14
 ACCH2N
 Nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
 C;Accession: S00377
 R;Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
 EMBO J. 7, 595-601, 1988
 A;Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptor subunit families
 A;Reference number: S00376; MUID:88283624; PMID:3267226
 A;Accession: S00377
 A;Molecule type: DNA
 A;Residues: 1-528 <NEF>
 A;Cross-references: EMBL:X07339; NID:G62792; PIDN:CAB59645.1; PID:G6136914
 C;Genetics:
 A;Introns: 21/1; 73/3; 88/3; 125/2; 487/3
 C;Superfamily: acetylcholine receptor
 C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
 F;241-264/Domain: transmembrane #status predicted <TM1>
 F;272-290/Domain: transmembrane #status predicted <TM2>
 F;306-327/Domain: transmembrane #status predicted <TM3>
 F;502-520/Domain: transmembrane #status predicted <TM4>
 F;54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;158-172,222-223/Disulfide bonds: #status predicted

Query Match 34.7%; Score 937.5; DB 1; Length 528;
 Best Local Similarity 37.8%; Pred. No. 7.9e-72;
 Matches 200; Conservative 85; Mismatches 175; Indels 69; Gaps 10;

QY 8 VWLAL-----AASLLHVSQGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMD 64
 DB 13 VWCFTVLTQATREQQKPHGAEDRLFKHLFTGYNRWRSPVNTSDVIVRFLSLAQILD 72
 QY 65 VDEKNQVLTNNIWLQMSQTHYLVQWVSEYPGVKTVPDPGQIWKPKDILLYNASDERFAD 124
 DB 73 VDEKNQMTNNVWLKQWSDYKLRWNPEDFNVTISIRVPSEMINIPDIVLYNADGEFAV 132
 QY 125 THTNVLNNSGHCQYLPPIGIFKSSCIDVYRWPPDVQHCCLKFGWSYSGWSLDLQWQE 184
 DB 133 THTKAHLFNGKVKWVPVPAIYKSSCIDVTFYFDDQCNCKMFGSWTYDKAKIDLENME 192
 QY 185 --ADISGYIPNGEWDLVGIPGKRSERFYECCKEPPYDVTFVTMRRTLYGLNLLIPCV 242

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: Juné 20, 2003, 19:00:32 ; Search time 52 Seconds
(without alignments)
1044.612 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 2703
Sequence: 1 MRCSPGVWLAASLLHVS.....TIGILMSAPNFVEAVSKDFA 502

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2703	100.0	502	9	US-09-954-936-2
2	2698	99.8	502	10	US-09-892-985-8
3	1254.5	46.4	501	10	US-09-303-232-6
4	1242	45.9	496	10	US-09-303-232-4
5	1155.5	42.7	770	10	US-09-303-232-2
6	959	35.5	622	10	US-09-941-179A-11
7	943	34.9	622	10	US-09-941-179A-3
8	933	34.5	502	9	US-10-157-031-92
9	928.5	34.4	631	10	US-09-941-179A-7
10	920.5	34.1	528	10	US-09-892-985-2
11	908	33.6	504	10	US-09-892-985-4
12	871.5	32.2	450	9	US-10-156-239-11
13	871.5	32.2	450	9	US-10-199-485-11
14	871.5	32.2	450	10	US-09-795-693-11
15	871	32.2	627	10	US-09-892-985-6
16	869	32.1	498	10	US-09-892-985-3
17	863.5	31.9	529	9	US-10-156-239-31
18	863.5	31.9	529	9	US-10-199-485-31
19	863.5	31.9	529	10	US-09-795-693-31

20	861	31.9	502	10	US-09-892-985-10	Sequence 10, Appl
21	842	31.2	457	9	US-10-157-031-28	Sequence 28, Appl
22	799	29.6	449	9	US-10-199-995-2	Sequence 2, Appl
23	621	23.0	520	9	US-10-012-542-144	Sequence 144, Appl
24	443.5	16.4	210	10	US-09-820-339A-2	Sequence 2, Appl
25	421	15.6	235	10	US-09-820-339A-6	Sequence 6, Appl
26	415	15.4	471	9	US-09-899-495-116	Sequence 116, Appl
27	413	15.3	230	10	US-09-820-339A-8	Sequence 8, Appl
28	395.5	14.6	447	10	US-09-955-524-9	Sequence 9, Appl
29	375	13.9	70	9	US-09-899-495-87	Sequence 87, Appl
30	373	13.8	441	10	US-09-732-680A-2	Sequence 2, Appl
31	294.5	10.9	132	9	US-09-899-495-86	Sequence 86, Appl
32	253.5	9.4	63	9	US-10-106-698-5644	Sequence 5644, Ap
33	232	8.6	485	10	US-09-808-483-12	Sequence 12, Appl
34	232	8.6	535	10	US-09-808-483-10	Sequence 10, Appl
35	210.5	7.8	440	9	US-09-510-662A-39	Sequence 39, Appl
36	210.5	7.8	440	10	US-09-778-320-39	Sequence 39, Appl
37	210.5	7.8	440	10	US-09-910-689-39	Sequence 39, Appl
38	210.5	7.8	440	12	US-10-010-742-39	Sequence 39, Appl
39	210.5	7.8	461	9	US-10-106-698-6308	Sequence 6308, Ap
40	208.5	7.7	417	9	US-10-075-846-2	Sequence 12, Appl
41	207.5	7.7	452	9	US-10-211-673-12	Sequence 12, Appl
42	202.5	7.5	357	9	US-09-899-495-118	Sequence 118, Appl
43	201.5	7.5	465	9	US-09-818-657-4	Sequence 4, Appl
44	197.5	7.3	431	9	US-10-075-846-4	Sequence 4, Appl
45	197.5	7.3	452	9	US-10-075-846-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match	100.0%;	Score 2703;	DB 9;	Length 502;
Best Local Similarity	100.0%;	Pred. No. 1.2e-251;		
Matches	502;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
Qy	1	MRCSPGVWLAASLLHVS	QGFQKLYKELVKNYNPLRPVANDSQPLTVTFSL	60
Db	1	MRCSPGVWLAASLLHVS	QGFQKLYKELVKNYNPLRPVANDSQPLTVTFSL	60
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Qy	121	RFDAFTNNVNLVNSGGHCQVLPPIFKSSCCVIDVWFPPFVQHCCKLFGSWSYGWSL	180	

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Db 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
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Db 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTHDEHL 420
Qy 421 LHGGQPEGDDPLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDDPLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 2

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US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US2002011463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8

Query Match          99.8%; Score 2698; DB 10; Length 502;
Best Local Similarity 99.8%; Pred. No. 3.7e-251;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRCSPGGVWALAAASLLHVSLSQGFQKLYKELVKNVPLRPVANDSQPLTVVFSLSLL 60
Db 1 MRCSPGGVWALAAASLLHVSLSQGFQKLYKELVKNVPLRPVANDSQPLTVVFSLSLL 60
Qy 61 QIMDVDEKNOVLTINILQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKNOVLTINILQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
Db 121 RFDAFHTNVLNNSGHCQYLPPIKSSCYIDVRWPPDPVQHCCKLKFGSWSYGGWSLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPKRSERFECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPDPDGSVGCGRMACSPTHDEHL 420
Qy 421 LHGGQPEGDDPLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPEGDDPLAKILEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
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Db 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 3

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US-09-303-232-6
; Sequence 6, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; insect acetylcholine receptor subunits
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; EARLIER FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 6
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-6

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Query Match          46.4%; Score 1254.5; DB 10; Length 501;
Best Local Similarity 48.4%; Pred. No. 3.7e-112;
Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;

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Qy 10 LALAASLLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESILLOIMDVDEKN 69
Db 8 LALLA-LLPVSEQEPHEKRLNALLNANTLERPVANESEPLEYRFGTLQOIIIDVDEKN 66
Qy 70 QVLTTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFDATFTN 129
Db 67 QLLITNIWLSLEWNYLNRWDSYGGVKDLRITPNKWKPDVLMYNSADEGFGDTQTN 126
Qy 130 VLNVSSGHCOYLPPGIFKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQE---AD 186
Db 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFPDDQCHDMKFGSWTYDGNQDLVLKDEAGD 186
Qy 187 ISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRLTYGLNLLIBCVLISA 246
Db 187 LSDFITNGEYLLGMPGKKNITTYACCEPYVDVFTIMIRRRRLTYFFNLIIVPCVLIS 246
Qy 247 LALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306
Db 247 MALLGFTLPPDSGEKLTGLVTIILSLTVFLNVAETLPOVSDAIPLLGTTFNCIMFWAS 306
Qy 307 SVVTVTVIVLQYHHDPDGGKMPKTRVILLNWCWFLMRKRPGBDKVRPACQHKQRCSL 366
Db 307 SVVTVTVVLYNYHRTADIEHPQWIKSVFLQWLPWILMRSPGKKITRKTIMMTRMREL 366
Qy 367 ASVMSAVA-----PPP-----ASGNLLYIGFRGLDGVHCVPTPDSGVVC 407
Db 367 ELKERSKSLANLVLDIDDDFRHGPPPPNSTAGNL-----GPGC 407
Qy 408 G-----RWACSPTHDELLHGGOPPEGPDGLAKILEEVRYIANFRCODESEAVCSEW 460
Db 408 STFRDTRRSFVRPSTWEDV--GGGLGSHREHLHLIRELOQFATRMKKADEAEALISDW 465
Qy 461 KFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
Db 466 KFAAMVVDRLCLVFTLFTIIATVAVLLSAPHII 499

RESULT 4
US-09-303-232-4
; Sequence 4, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-303-232-4

Query Match 45.9%; Score 1242; DB 10; Length 496;
Best Local Similarity 45.8%; Pred. No. 5.8e-111;
Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

Qy 4 SPGWVWLAASLLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESILLOIM 63
Db 12 APAGLLLLCLLWPRGARGCYHEKRLHLHLHDHYNVLERPVNESDPLQSLFGLTLMQII 71
Qy 64 VDDEKNQVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFD 123
Db 72 VDDEKNQVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFD 131
Qy 124 ATFTHTNLVNSGHCOYLPPGIFKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQ 183
Db 132 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCCEMKGFSWTYDGYQLDLQLQ 191

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Qy 184 E---ADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRLTYGLNLLIP 240
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Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 252 CVLIASMALGFTLPPDSGEKLSLGTIILSLTVFLNVAETMPATSDAVPLGTYFNCI 311
Qy 301 MIIVGLSVVTVIVLQYHHDPDGGKMPKTRVILLNWCWFLMRKRPGBDKVRPACQHK 360
Db 312 MFWASSVVSITILINHYHRHADTHEMSDWIRCVFLYWL PWVLRMSRPG----- 360
Qy 361 QRRCSLASVMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPH---- 416
Db 361 -----SATTPPPAR-----VPPPPDLELRERSSKSLANVLD 392
Qy 417 -DEHLH-----CGQPPEG-----DPDLAKILEEVRYIANFRCODE 452
Db 393 IDDDFRHPQAQOQPCRYRGEENGAGLAASHCFGVDYELSLILKEIRVITDQMRKODE 452
Qy 453 SEAVCSEWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFV 494
Db 453 DADISRDKWKAAMVVDRLCLLIIFTLIIATLAVLLSAPHIM 494

RESULT 5
US-09-303-232-2
; Sequence 2, Application US/09303232A
; Patent No. US20020006657A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Nucleic Acids which encode
; FILE REFERENCE: Le A 33 020-Foreign Countries
; CURRENT APPLICATION NUMBER: US/09/303,232A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: DE 198 19 829.9
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-303-232-2

Query Match 42.7%; Score 1155.5; DB 10; Length 770;
Best Local Similarity 45.0%; Pred. No. 2.3e-102;
Matches 236; Conservative 82; Mismatches 116; Indels 91; Gaps 12;

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Qy 8 VWLALAASLLHVSLOGEFORGLYKELVKNYNPLERPVANDSOPLTVYFESILLOIMDYDE 67
Db 297 IYLNLSAK---VCLAGYHEKRLHLHLDPDPTLERPVNLNSDPLQLSFLGLTLMQIIDYDE 353
Qy 68 KNOVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFDATFH 127
Db 354 KNOVLTNIWLOMSWTDHYLQWNVSEYPGVKTFRFPDGOIWKPDIIILYNSADERFDATFH 413
Qy 128 TNVLVNSGHCOYLPPGIFKSSCYIDVRWFPDVOHQCKLKFGWSYGGWSLDLQWQE--- 184
Db 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCCEMKGFSWTYDGFQLDLQODETG 473
Qy 185 ADISGYIPNGEWDLVGIPGKRSERFECCKEYPDVTFTVMRRRLTYGLNLLIPCVLI 244
Db 474 GDISSVYLVNGEWELLGVPGKNEIYYNCCPEYIDITFAIIRRTTYFFNLIIPCVLI 533
Qy 245 SALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFTMIIV 304
Db 534 ASMALGFTLPPDSGEKLSLGTIILSLTVFLNVAETMPATSDAVPL----- 581
Qy 305 GLSVVTVTVIVLQYHHDPDGGKMPKTRVILLNWCWFLMRKRPGBDKVRP-ACQHKORR 363

```

Db 582 -----WIRIVFLCWLFWILRMSRPG-----RPLILEPPTTP 612
 Qy 364 CSLASVE-----MSAVAPPPASGNLLY-----IGRGLDGVHCVp-TP-----401
 Db 613 CSDTSSERKHQILSDVELKERSKSLANVLDDDFRH-----NCRPMTGGTLPHNPAF 668
 Qy 402 -----DSGVV-----CGRMACSPTHDEHLHGGQPPGEGDPLAKILEVRVYANRFR 449
 Db 669 YRTVYQGGDGSIGPIGSTRMPDAVTH-----HTCIKSSTSEYELGLILKEIRITDQLR 723
 Qy 450 QDESEAVCSEWFAACVDRCLMAFSVFTIICIGILMSAPNFV 494
 Db 724 DDECNDIANDWKEFAAMVVDRLCLIFTFMFAILATIAVLLSAPHII 768

RESULT 6

US-09-941-179A-11
 ; Sequence 11, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-11

Query Match 35.5%; Score 959; DB 10; Length 622;
 Best Local Similarity 34.3%; Pred. No. 1.4e-83;
 Matches 209; Conservative 90; Mismatches 186; Indels 124; Gaps 9;
 Qy 4 SPGGVWLALASLL-----HVSLOGEFQKLYKELVKVKNYPLERPVANDSOPLTIVYFSL 59
 Db 6 SKGNLLLLLCASIFPAFGHVETRAHAERLLKLFSGYNKWSRPVANISDVVLVRFGLSI 65
 Qy 60 LQIMDVDEKNOVLTTNIWLQMSWTDHYLQWNSVEYPGVKTVPDPGQIWKPDILLYNSAD 119
 Db 66 AQLIDVDEKNOVMTTNVVWQKQWHDYKLRWDPOEYENVTSIRIPSELIRWPDIVLYNNAD 125
 Qy 120 ERDATHTNVLNNSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCKLFGSWSYGGWSLD 179
 Db 126 GDFAVTHLTKAHLFYDGRIRKMPAPAIYKSSCIDVTFPPDQCKMKFGSWTYDKAKID 185
 Qy 180 L--QMEADISGYPNGEWDLVIGPKRSERFECCKEPPDYDTFTVTRRTLYYGLNL 237
 Db 186 LVSMHSHVDLSEFYTSVEWDLVPAVRNEKFTYCCDEPYLDITFNFIIRRLPLFYTNL 245
 Qy 238 LIPCVLISALALLVFLPLPADSGEKISLIGITVLLSTTFMLLVAIMPATSDSVPLIAQYF 297
 Db 246 IIPCLLISCLTVLVFVLPSCGEEKITLCISVLLSLTVFLLITETIIPSTSLVIPLEIYL 305
 Qy 298 ASTMIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNCAWFLRMKRFPG-----349
 Db 306 LFTMIFVTLISIIITVFLNVHRSRPTHMPDWVRRVFLDIVPRLLFMKRPSTVKDNCKK 365
 Qy 350 -----EDKVRPACQHKOR 362
 Db 366 LIESMHLKLTNSPRLMSETDMEPNFTSSPSQSNPSPTSSFCALHEEPKMPCKSPSG 425
 Qy 363 RCSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393

Db 426 QYSMHLPEPPQVTCSSPKPSCHPLSDTQTTSISKGRSLSVQOQMYSPNKNTEGSTRCSRS 485
 Qy 394 GVHCVPPTDSGVVCGRMACSPT-----HDEHLH-----GGQPEP-----429
 Db 486 IQCYILOEDSSQTNHSSASPASQRCILNEEQPHKPHQCKCKRKGAEAGTPTQGSKSH 545
 Qy 430 -----DPLAKILEVRVYANRFRQDSEAVCSEWFAACVVDRLCLMAFSVFT 479
 Db 546 SNKGEHLVMSLPALKLAVEGVHYADHLRAEDADFSVKEDWKYVAVIDRIFLWFIIVC 605
 Qy 480 IICITIGILM 488
 Db 606 LLGTVGLFL 614

RESULT 7

US-09-941-179A-3
 ; Sequence 3, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-3

Query Match 34.9%; Score 943; DB 10; Length 622;
 Best Local Similarity 33.7%; Pred. No. 5e-82;
 Matches 205; Conservative 91; Mismatches 189; Indels 124; Gaps 9;
 Qy 4 SPGGVWLALASLL-----HVSLOGEFQKLYKELVKVKNYPLERPVANDSOPLTIVYFSL 59
 Db 6 SKGNLLLLLCASIFPAFGHVETRAHAERLLKLFSGYNKWSRPVANISDVVLVRFGLSI 65
 Qy 60 LQIMDVDEKNOVLTTNIWLQMSWTDHYLQWNSVEYPGVKTVPDPGQIWKPDILLYNSAD 119
 Db 66 AQLIDVDEKNOVMTTNVVWQKQWHDYKLRWDPOEYENVTSIRIPSELIRWPDIVLYNNAD 125
 Qy 120 ERDATHTNVLNNSGHCQYLPPIPKSSCYIDVRWPPFDVQHCCKLFGSWSYGGWSLD 179
 Db 126 GNFEVTLATKATLNTVGRVWRPAPAIYKSSCIDVVEYFPDQCTCMKFGSWTYDKAKID 185
 Qy 180 LQMEADIS--GYIPNGEWDLVIGPKRSERFECCKEPPDYDTFTVTRRTLYYGLNL 237
 Db 186 LVSMHSHVDLQDYWESGEWVIINAVGNYSKKYCCCTEIPDITVFIIRRLPLFYTNL 245
 Qy 238 LIPCVLISALALLVFLPLPADSGEKISLIGITVLLSTTFMLLVAIMPATSDSVPLIAQYF 297
 Db 246 IIPCLLISCLTVLVFVLPSCGEEKITLCISVLLSLTVFLLITETIIPSTSLVIPLEIYL 305
 Qy 298 ASTMIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNCAWFLRMKRFPG-----349
 Db 306 LFTMIFVTLISIIITVFLNVHRSRPTHMPDWVRRVFLDIVPRLLFMKRPSTVKDNCKK 365
 Qy 350 -----EDKVRPACQHKOR 362
 Db 366 LIESMHLKLTNSPRLMSETDMEPNFTSSPSQSNPSPTSSFCALHEEPKMPCKSPSG 425
 Qy 363 RCSLASVE---MSAVAPPPA-----SNGNLL-----YIGFRGLD 393

Db 426 QYSLHPEPPQVTCSSPKPSCHPLSDTQTTSISKGRSLSVOQMSPNKTBEGSIRCRSRS 485
 QY 394 GVHCVTPTDGSVCGRMACGPT-----HDEHLLH-----GGQPPEG----- 429
 Db 486 IOCYLQEDSSQTNHSSASPASQORCHLNEEQPKHQCKCKRCKGEAAGTPTQGSKSH 545
 QY 430 -----DPLAKLIEEVRYIANRFRCODESEAVCESEVCKFAACVDRCLCLMAFSVFT 479
 Db 546 SNKGEHLVMSLPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRIFLWMFIIVC 605
 QY 480 IICTIGILM 488
 Db 606 LLGTGVLGL 614

RESULT 8

US-10-157-031-92
 ; Sequence 92, Application US/10157031
 ; Publication No. US20030108890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baranova, A. V.
 ; APPLICANT: Yankovsky, N. K.
 ; APPLICANT: Kozlov, A. P.
 ; APPLICANT: Lobashev, A. V.
 ; APPLICANT: Krukovskaya, L. L.
 ; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
 ; FILE REFERENCE: 2760-103
 ; CURRENT APPLICATION NUMBER: US/10/157,031
 ; CURRENT FILING DATE: 2002-05-30
 ; NUMBER OF SEQ ID NOS: 415
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 92
 ; LENGTH: 502
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-157-031-92

Query Match 34.5%; Score 933; DB 9; Length 502;
 Best Local Similarity 37.7%; Pred. No. 3.4e-81;
 Matches 189; Conservative 92; Mismatches 166; Indels 54; Gaps 7;
 QY 10 LALAASLLHVSLOGEFQRLKYLKVNKNYPLRPVANDSOPLTIVYFSLSLQIMVDENK 69
 Db 16 LLLLSLLPVARASEAERLFFERLFEDYNEIIRPVANVSDPVIHFVMSQLVKVDEVN 75
 QY 70 QVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSADERPDATHTN 129
 Db 76 QIMETNLWLQIMNDYKLNWPSGYGGAEMRVPQAOKIWKPDIVLYNNVAGDFQVITTK 135
 QY 130 VLNVSSGHQYLLPPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSLDQM--QEADI 187
 Db 136 ALLKYTGVTWTPPAIFKSSCKIDVTYFPDYQNCYTKMFGSWSYDKAKIDLVIGSMNL 195
 QY 188 SGYIPNGEWDVGIPOKRSERFYECCKEYPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
 Db 196 KDYWESGEWAIKAPGYKDKIKYNCCEIYPDITYSLYSRRLPLFYTNILIPCLLISFL 255
 QY 248 ALLVFLPADSGEKISGITVLLSTFTMLVAEIMPATSDSVPLIAQYFASVTMIIVGLS 307
 Db 256 TVLVFVLPDSCGEKVTLCISVLLSLVFLVAVITETIPSTSLVPLIGEYLLFTMIFTLS 315
 QY 308 VVVTVLVQYHHDPDGGKMPKWTIRVILLNWCWFLRMKPEGDKYRPAQCHKQRRCSLA 367
 Db 316 IVITVFLNVHRTPTTHMPSVWTKVFLMLLPRVFMFTRP-----T 357
 QY 368 SVMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDS-----GVVCGRMACSPTHDEHL-- 420
 Db 358 SNEGNAQKRPPLYGAE-----LSNLNCFSAESKGEKGYPCQDGMCGYCHRRIKI 409
 QY 421 -----LHGQDPEG-----DPLAKLIEEVRYIANRFRCODESEAVCESEVCKFAA 464
 Db 410 SNFSANLTRSSSESVDVAVVSLSALSPEIKAEIQSVKYIAENMKQAQNEAKEIQDDWKYVA 469

QY 465 CVVDRLCLMAFSVFTIICTIG 485
 Db 470 MVIDRIFLW---VFTLVCLIG 487

RESULT 9

US-09-941-179A-7
 ; Sequence 7, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-7

Query Match 34.4%; Score 928.5; DB 10; Length 631;
 Best Local Similarity 33.3%; Pred. No. 1.3e-80;
 Matches 206; Conservative 90; Mismatches 189; Indels 133; Gaps 9;
 QY 4 SPGCVMLALAASLL-----HVSLOGEFQRLKYLKVNKNYPLRPVANDSOPLTIVYFSL 59
 Db 6 SKGNLLLLLCASIPPAFGHVETRAHAERLLKLPFGSKYKNSRPNVANISDVVLVRFGLSI 65
 QY 60 LQIMDVDEKQVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSAD 119
 Db 66 AQLIDVDEKQVLTNNIWLQMSWDHYLQNVSEYPCVKTVPDGOIKWPDILLNYSAD 125
 QY 120 ERFDATHTNNVNSSGHQYLLPPGIFKSSCYIDVRWFPDVOHQCKLFGSWSYGGWSLD 179
 Db 126 GDFAVTHLTKAHLFYDGRKIKWMPPIAYKSSCIDVTFFPFQONCKMFGSWYDKAKID 185
 QY 180 LQMQEA-----DISGYIPNGEWDVGIPOKRSERFYECCKEYPDVTFTVWTR 228
 Db 186 LVSMHSHRGTVNVVELGVDQLDYWESGEWIIINAVGNYSKKYECCTETYPDITYSFIIR 245
 QY 229 RTLYYGLNLLIPCVLISALALLVFLPADSGEKISGITVLLSTFTMLVAEIMPATSD 288
 Db 246 LPFYTNNILIPCLLISCLTVLVFYLSECEKVTLCISVLLSLTVFLLLTETIIPSTSL 305
 QY 289 SVPLIAQYFASVTMIIVGLSVVVTVVILQYHHDPDGGKMPKWTIRVILLNWCWFLRMKRP 348
 Db 306 VIPLIGEYLLFTMIIVTLSIIITVFLNVHRSRTHMTPDVRVFLDIVPRLLFMKRP 365
 QY 349 G-----EDKV 353
 Db 366 STVKDNCKLIESMHKLTNSPRLMSETDMEPNFTTSSSPSPQSNPEPSTSSFCARLEP 425
 QY 354 RPACQHKQRCSLASVE--MSAVAPPA-----SNGNLL----- 385
 Db 426 KPMCKSPSGYSLMLHPEPPQVTCSSPKPSCHPLSDTQTTSISKGRSLSVOQMSPNKTBEE 485
 QY 386 -YTGFRGLDGVHCVPTPDSGVVCGRMACSP-----HDEHLLH-----GG 424
 Db 486 GSIRCRSRSIOYCYLQEDSSQTNHSSASPASQORCHLNEEQPKHQCKCKRCKGEAAG 545
 QY 425 QPPEG-----DPLAKLIEEVRYIANRFRCODESEAVCESEVCKFAACVVDRL 470
 Db 546 TPTQGSKSHNKGEHLVMSLPALKLAVEGVHYIADHLRAEDADFSVKEDWKYVAMVIDRI 605

QY 471 CLMAFSVFTIICITIGILM 488
 Db 606 FLWFIIVCLLGTGVLFL 623

RESULT 10

US-09-892-985-2
 ; Sequence 2, Application US/09892985
 ; Patent No. US20020111463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; Ellis, Steven B.
 ; Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heller Ehrman White & McAuliffe
 STREET: 4250 Executive Square, 7th Floor
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/892,985
 FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/466,589,
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9949B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-450-8400
 TELEFAX: 619-587-5360
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 528 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-892-985-2

Query Match 34.1%; Score 920.5; DB 10; Length 528;
 Best Local Similarity 39.4%; Pred. No. 5.8e-80;
 Matches 198; Conservative 77; Mismatches 162; Indels 65; Gaps 10;

QY 24 EFORKLYKELVKNYPLERVANDSQPLTVYFSLSLQIMDVDEKQVLTNINLQMSWT 83
 Db 57 ETEDLFLFKLFGYRNWRPVPNTSDVIVRFGLSIAQLIDVDEKQVMTTNVLKQWS 116
 QY 84 DHVLYQNVSEYPGVKTVPFDGQITWKEDILLVNSADERFDTFTNVLVNSSGHCQVLP 143
 Db 117 DYKLRWNPDGNGITSILRVSEMIWIDIVLVNXXGE-FAYTHMTKAHLFSTGTGVHWVPP 175
 QY 144 GIFKSSCYIDVRFPFDPQVQKLFKFGSWSGWGLDLQMQE--ADISGYINPGEWDLVGI 201
 Db 176 AIYKSSCIDVTFFPDPQCKKFKGWSWTYDKAKIDLEQMEQTVDLKDYWESGEWAIYNA 235

QY 202 PKRSERFYECCKEYPDPVTFTVMRRRTLYYGLNLLIPCVLISALALLVFLPADSGEK 261
 Db 236 TGYNSKKYDCCAEIYPDVTYAFVIRRLPLFYTNILIIICLLISCLTVLVFYLPSDCGEK 295
 QY 262 ISLGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASWTMIIVGLSVVVTVIVLYOHHHD 321
 Db 296 ITCISVLLSLTFTMLLVAEIMPATSDSVPLIAQYFASWTMIIVGLSVVVTVIVLYOHHHD 355
 QY 322 PDGKMPKTRVILLNWCAMFLMRKRGEDKVRPACQHKQRCSLASVENSVAVPPASN 381
 Db 356 PSTHTMHWVRGALLGCVPRWLLMNR-PPPVVEL 388
 QY 382 GNLLIY----GFRGLDG-----VHCVPPTDPSGVWQGRMA-----CSPTHDEHLLHGG 424
 Db 389 CHPLRLKLSFYHWSNVDABEREVVVEEDRWACAGHVAPSVGTLCSHGH-----LHSG 444
 QY 425 QP-----PEGD-----PDLAKILEVRVIANFRCODESEAVCSEWKFACVVDRLCL 472
 Db 445 ASGPKAEALLQEGELLSPHMQKALEGVHIADHLRSEDADSSVKEDWKYVAMVIDRIFL 504
 QY 473 MAFSVFTIICITIGILMSAPNFV 494
 Db 505 WLFIIVCFLGTIGLFL--PPFL 524

RESULT 11

US-09-892-985-4
 ; Sequence 4, Application US/09892985
 ; Patent No. US20020111463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliot, Kathryn J.
 ; Ellis, Steven B.
 ; Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heller Ehrman White & McAuliffe
 STREET: 4250 Executive Square, 7th Floor
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/892,985
 FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/466,589,
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9949B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-450-8400
 TELEFAX: 619-587-5360
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 504 amino acids
 TYPE: amino acid

RESULT 12

ORGANISM: Homo sapiens
US-10-199-485-11

Query Match 32.2%; Score 871.5; DB 9; Length 450;

Best Local Similarity 38.2%; Pred. No. 2.4e-75;

Matches 187; Conservative 81; Mismatches 164; Indels 57; Gaps 7;

```
QY 12 LAASLLHVSLL-----QGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIM 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 LSLGILLLSLLPAECLGAEGLALKLFRDLFANYTSALRPVADTQTLNVTLEVTLSQII 67
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 DVDEKNOVLTTNIWLQMSWTDHYLQNVSEYPGVKTVRFPDGGQIKWPKDILLYNSADRFD 123
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 DMDEKNOVLTLWLIRQWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIIVLYNKADAQPP 127
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 ATFTHTNLVNSSGHCQYLPPIKSSCIYIDVRWFFPDVQHCCKLKFGSWSYGGWSLDLQMQ 183
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 GSASTNNVLVRHGDGAVRWDAIPATIRSSCRVDVAAFPFDAQHCGLTFGSWTHGHQDLVRPR 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 --EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIPC 241
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 GAAASLADFVENVEWVRLGMPARRVLTGCCSEYPDVTFTLLRRRAAYVNCNLLIPC 247
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 VLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFM 301
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 VLISLAPLAFHLPADSGEKVSLGVTVLLALTVPQLLAESMP-PAESVPLIGKYYMATM 306
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 IIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRGEDKVRPACQHKQ 361
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 TMTFTSTALTILIMNLHYCGPSVRPVPAMARALLGLHARGLCVRERGE----PCGQSRP 362
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 RRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDEHLL 421
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 363 PELSPSPQSPGAGPAG-----PCHEPRCLC-----RQALL 396
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 HGGQPPGPDPAKILEEVRYIANRFRCDSEAVCSEWKFACVDRCLCLMAFSVFTII 481
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 397 H-----HVATIANFRSHRAAQCHEDWKRLARVMDRFFLAIFFSMALV 440
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 CTIGILMSA 490
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 441 MSLVLVQA 449
```

RESULT 14

US-09-795-693-11

Sequence 11, Application US/09795693

Patent No. US20020068710A1

GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria A.

TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and

FILE REFERENCE: 32613, No. US20020068710A1 Human Transporters

CURRENT APPLICATION NUMBER: US/09/795,693

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 450

TYPE: PRT

ORGANISM: Homo sapiens

US-09-795-693-11

Query Match

Best Local Similarity 32.2%; Score 871.5; DB 10; Length 450;

Matches 187; Conservative 81; Mismatches 164; Indels 57; Gaps 7;

```
QY 12 LAASLLHVSLL-----QGEFORKLYKELVKNYNPLERPVANDSOPLTIVYFSLSLQIM 63
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 LSLGILLLSLLPAECLGAEGLALKLFRDLFANYTSALRPVADTQTLNVTLEVTLSQII 67
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 64 DVDEKNOVLTTNIWLQMSWTDHYLQNVSEYPGVKTVRFPDGGQIKWPKDILLYNSADRFD 123
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 68 DMDEKNOVLTLWLIRQWTDAYLRWDPNAYGGLDAIRIPSSLVWRPDIIVLYNKADAQPP 127
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 ATFTHTNLVNSSGHCQYLPPIKSSCIYIDVRWFFPDVQHCCKLKFGSWSYGGWSLDLQMQ 183
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 GSASTNNVLVRHGDGAVRWDAIPATIRSSCRVDVAAFPFDAQHCGLTFGSWTHGHQDLVRPR 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 --EADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRRTLYYGLNLLIPC 241
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 GAAASLADFVENVEWVRLGMPARRVLTGCCSEYPDVTFTLLRRRAAYVNCNLLIPC 247
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 VLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASFM 301
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 VLISLAPLAFHLPADSGEKVSLGVTVLLALTVPQLLAESMP-PAESVPLIGKYYMATM 306
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 IIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRGEDKVRPACQHKQ 361
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 TMTFTSTALTILIMNLHYCGPSVRPVPAMARALLGLHARGLCVRERGE----PCGQSRP 362
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 362 RRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPHDEHLL 421
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 363 PELSPSPQSPGAGPAG-----PCHEPRCLC-----RQALL 396
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 HGGQPPGPDPAKILEEVRYIANRFRCDSEAVCSEWKFACVDRCLCLMAFSVFTII 481
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 397 H-----HVATIANFRSHRAAQCHEDWKRLARVMDRFFLAIFFSMALV 440
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 CTIGILMSA 490
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 441 MSLVLVQA 449
```

RESULT 15

US-09-892-985-6

Sequence 6, Application US/09892985

Patent No. US20020111463A1

GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

Ellis, Steven B.

Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/892,985

FILING DATE: 27-Jun-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/217,345

FILING DATE: 21-DEC-98

APPLICATION NUMBER: US 08/467,574

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/466,589,

FILING DATE: 05-JUN-95

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 24735-9949B

TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-892-985-6

Query Match      32.2%; Score 871; DB 10; Length 627;
Best Local Similarity 33.1%; Pred. No. 4.3e-75;
Matches 202; Conservative 86; Mismatches 184; Indels 138; Gaps 11;

QY 10 LALAASLL-----HVSLOGEQKLYKELKKNYNPLERPVANDSQPLTVYFSLSLLOIMDV 65
Db 17 LLGTLGRASSHVETRAHAERLLKLLFGYNKWSRPVANISDVLRFLGSLIAQLIDV 76

QY 66 DEKNQVLTINILWOMSTHYLQWNVSEYPCGKTVRFPGQIWKPDILLNYSADERFDAT 125
Db 77 DEKNQMTTNVVKQEHYKLRWDPADYENVTSIRIPSELINRPDIALYNNADGDFAT 136

QY 126 FHTNLVNSGHCQYLPPIGFKSSCYIDVRWFFDVQHCCLKFGSWSYGGWSLDEL--QM 183
Db 137 HLTKAHLFDRGVORTPTPAIYKSSCIDVTFPPDQNCNWKFGSWTYDKAKIDLNVNHS 196

QY 184 EADISGYPNGEWDLVCIPIGKRSEFYECCKEPPYDVTFTVTRRRRTLYGLNLLIPC 243
Db 197 RVDQLDFWEGEMLIADAXGTYNTRKYECCEAIYPDITYAYAIRRLPLFCTINILIP 256

QY 244 ISALALLVFLPADSGEKISLIGITVLLSLTFTMLLVAEIMPATSDSVPLIAQYFAS 303
Db 257 ISCLTALVFLPSCGCKITLCISALLSLTGLLITLITPTSLVPLIGEYLLFTMIF 316

QY 304 VGLSVVVTIVLQYHHHDPDGGKMKWTRVILLNWCALFEMKPEGDKVRPACQHKORR 363
Db 317 VTLSIAITVFLNVVHHSRTHMTPTWVRSVFLDIVPRLLLMKEP--SVVKDNC---R 369

QY 364 CSLASVEMSAVAP-----PPASNG----- 382
Db 370 RLIESMHKMASAPRFWPEPEGEPPATSGTOSLHPPSPFCVPLDVPAEPGPKSPSQ 429

QY 383 -----NLLYIGRG--LDG----- 394
Db 430 PPQKPLEAEKDSPPSPGCRPHGTOAPGLAKARSLVQHMSSPGEAVGGVRCRSRI 489

QY 395 VHCVPPTDS-----GVVCGRMACSPTHDEHLLHGGQP-----PEG----- 429
Db 490 QYCVPRDDAAPEADGQXAGLASENSHAELPPPDQSPCKCTCKEPPSSVPSAXVKTR 549

QY 430 -----DPDLAKILEVRYIANFRQDSEAVCSSEWKFACVDRCLCLMAFSVF 478
Db 550 STKAPPPHPLSPALSRAVEGVQYADHLKAEDTDFSVKEDWKYVANVIDRIFLWMFI 609

QY 479 TIICTIGILM 488
Db 610 CLLGTVGLFL 619
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Search completed: June 20, 2003, 19:10:17
Job time : 55 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2003, 18:50:16 ; Search time 73 Seconds
(without alignments)

916.326 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 2703

Sequence: 1 MRCSPGVWIALAASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	502	19 AAW69216	V274T variant huma
2	2698	99.8	502	15 AAW44153	Human neuronal nic
3	2698	99.8	502	18 AAW09025	Neuronal nicotinic
4	2698	99.8	502	21 AAB24088	Human PRO2145 prot
5	2698	99.8	502	22 AAB82690	Nicotinic acetylch
6	2698	99.8	502	22 AAB50012	Wild-type human al
7	2692	99.6	502	22 AAB50015	Mutant human alpha
8	2688	99.4	502	22 AAB50016	Mutant human alpha
9	2682	99.2	502	22 AAB50017	Mutant human alpha
10	2429	89.9	502	18 AAW12368	Neuronal alpha-bun

11	1816.5	67.2	511	18 AAW12369	Neuronal alpha-bun
12	1474.5	54.6	470	22 AAB50014	Chimeric alpha7/5-
13	1360.5	50.3	448	22 AAB50018	Mature cell surfac
14	1254.5	46.4	501	21 AAY50816	H. virescens acety
15	1242	45.9	496	21 AAY50815	D. virescens acety
16	1155.5	42.7	770	21 AAY50814	D. melanogaster ac
17	1088	40.3	554	22 AAE12824	Caenorhabditis ele
18	975.5	36.1	631	23 AAO17243	Modified acetylcho
19	959	35.5	622	23 AAO17245	Modified acetylcho
20	959	35.5	622	23 ABB08885	Modified hen ACR s
21	954	35.3	311	22 ABB63683	Drosophila melanog
22	945	35.0	529	15 AAW44155	Human neuronal nic
23	945	35.0	529	16 AAR73966	Alpha 2 subunit of
24	945	35.0	529	18 AAW09021	Neuronal nicotinic
25	945	35.0	529	23 ABB61850	Prostate cancer-as
26	943	34.9	622	23 AAO17242	Modified acetylcho
27	943	34.9	622	23 ABB08883	Insect nicotinic A
28	935.5	34.6	576	22 ABB61954	Drosophila melanog
29	932	34.5	504	18 AAW09022	Neuronal nicotinic
30	928.5	34.4	631	23 AAO17244	Modified acetylcho
31	928.5	34.4	631	23 ABB08884	Modified hen ACR s
32	925.5	34.2	580	22 ABB62727	Drosophila melanog
33	917	33.9	502	22 AAB51021	JTF-38 nAChr alpha
34	916	33.9	627	18 AAW11824	Alpha4 subunit of
35	916	33.9	627	18 AAW09023	Neuronal nicotinic
36	913	33.8	495	11 AAR07143	Neuronal nicotinic
37	913	33.8	627	18 AAW11825	Alpha4 subunit of
38	887	32.8	772	15 AAW44152	Human neuronal nic
39	886	32.8	722	22 ABB59012	Drosophila melanog
40	884	32.7	498	18 AAW09027	Neuronal nicotinic
41	882	32.6	504	15 AAW44156	Human neuronal nic
42	881	32.6	498	15 AAW44154	Human neuronal nic
43	877	32.4	521	22 ABB70062	Drosophila melanog
44	871.5	32.2	450	22 AAG67161	Amino acid sequenc
45	867.5	32.1	433	22 AAW00402	Mature human alpha

ALIGNMENTS

RESULT 1
AAW69216
ID AAW69216 standard; Protein: 502 AA.
XX
AC AAW69216;
XX
DT 09-OCT-1998 (first entry)
XX
DE V274T variant human alpha7 nAChr protein.

Alpha7 nAChr: alpha7 nicotinic acetylcholine receptor subunit; cancer;
neurodegeneration; enzyme dysfunction; affective disorder; therapy;
immune dysfunction; diabetic neuropathy; Alzheimer's disease;
schizophrenia.

OS Homo sapiens.

XX

FN WO9828331-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US23405.

XX

PR 20-DEC-1996; 96US-0771737.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

PI Roch J, Sullivan JP, Touma E;

XX

DR WPI; 1998-377593/32.

DR N-PSDB; AAV44687.

XX

PT Nucleic acid encoding variant of human alpha7 nicotinic
PT acetylcholine receptor sub-unit - used to identify modulators of
PT the receptor, potentially useful for treating neuro-degeneration,
PT cancer, affective disorders etc.
XX
PS Claim 15; Fig 2; 44pp; English.
XX
CC This sequence is the V247T variant of human alpha7 nicotinic
CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
CC the DNA are used to express the protein and to identify modulators of
CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
CC compounds or antagonists that are potentially useful for treating
CC neurodegeneration, enzyme dysfunction, affective disorders and immune
CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridisation or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
CC retained.
XX
SQ Sequence 502 AA;

Query Match 100.0%; Score 2703; DB 19; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.6e-260;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
Db |||||
QY 61 QIMVDKQVLTNTIWLQMSWDTHYLQNVSVYGVKTVRFPDQIWKPDILLYNSADE 120
Db |||||
QY 121 RDATEHTNVLNNSGHCQVLPFGIFKSSCYIDVRWFPDVOHCKLFGSWSYGGNSLDL 180
Db |||||
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSRFRFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
Db |||||
QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db |||||
QY 301 MIIVGLSVVTVTVLQYHHHPDGGKMPKTRVILLNWCWFLMKRPGEDKVRPACQHK 360
Db |||||
QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPDPDSVGVCGRMACSPTHDEHL 420
Db |||||
QY 421 LHGGQPEGDPDLAKILEEYRIYANRRFCQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db |||||
QY 481 ICTIGILMSAPNFEAVSKDFA 502
Db |||||

RESULT 2
AAW44153
ID AAW44153 standard; Protein; 502 AA.
XX
AC AAW44153;
XX

DT 14-MAY-1998 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
XX
XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
XX brain tissue; screening; NACHR; antibody.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX Domain /label= signal
XX /label= TMD1
XX /note= "transmembrane domain"
XX Domain 262..284
XX /label= TMD2
XX /note= "transmembrane domain"
XX Domain 290..317
XX /label= TMD3
XX /note= "transmembrane domain"
XX Misc-difference 343
XX /note= "encoded by CTS"
XX Domain 462..487
XX /label= TMD4
XX /note= "transmembrane domain"
XX Domain 318..461
XX /label= cytoplasmic_loop
XX
XX W09420617-A2.
XX
XX 15-SEP-1994.
XX
XX 08-MAR-1994; 94WO-US02447.
XX
XX 08-MAR-1993; 93US-0028031.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Elliott KJ, Ellis SB, Harpold MM;
XX
XX WPI; 1994-303024/37.
XX N-PSDB; AAV12197.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
XX also transformed cells useful for screening cpds. which modulate
XX activity of the receptor
XX
XX Claim 7; Page 80-81; 99pp; English.
XX
XX The present sequence represents a human neuronal nicotinic acetylcholine
XX receptor (NACHR) subunit. The cells expressing the alpha and/or beta
XX NACHR subunits may be used in a method of screening compounds to
XX identify any which modulate the activity of human neuronal NACHR.
XX Subunit specific antibodies may be used to monitor the distribution
XX and expression density of various subunits in normal vs diseased brain
XX tissues. Testing of single receptor subunits or specific receptor
XX subunit combinations with a variety of potential agonists or antagonists
XX provides information with respect to the function and activity of the
XX individual subunits and should lead to the identification and design of
XX compounds that are capable of very specific interaction with one or
XX more receptor subtypes. The resulting drugs should exhibit fewer
XX unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
XX
XX Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 15; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60

```

Db      1  MRCSFGVWLAALASLLHVSLSQGEFQRLKYKELVKNYNPLRPVANDSQPLTVVPSLSLL 60
QY      61  QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db      61  QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY      121  RFDATEHTNNVLNVSNGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWSLDL 180
Db      121  RFDATEHTNNVLNVSNGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWSLDL 180
QY      181  QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVDTFTVMRRRTLYYGLNLLIP 240
Db      181  QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVDTFTVMRRRTLYYGLNLLIP 240
QY      241  CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY      301  MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
QY      361  QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRWACSPTHDEHL 420
Db      361  QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRWACSPTHDEHL 420
QY      421  LHGGQPEGPDLLAKILLEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPEGPDLLAKILLEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

```

RESULT 3

AAW09025
ID AAW09025 standard; Protein; 502 AA.

AC AAW09025;

XX 09-APR-1997 (first entry)

XX Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
XX ligand-gated receptor.

XX Homo sapiens.

XX WO9641876-A1.

XX 27-DEC-1996.

XX 07-JUN-1996; 96WO-US09775.

XX 07-JUN-1995; 95US-0484722.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Harpold MW;

XX WPI; 1997-065463/06.

XX N-PSDB; AAT48239.

XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
XX used in screening to determine the effect of drugs on the receptor

XX Disclosure; Page 73-74; 108pp; English.

XX The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
XX acetylcholine receptor (nAChR) can be expressed in transformed

CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
CC cells, esp. mammalian cells or amphibian oocytes, expressing the
CC recombinant alpha-7 subunit, opt. in combination with other
CC recombinant alpha and/or beta subunits (see also AAW09018-24,
CC AAW09026-27), can be used to examine the function of human AChR and
CC to identify cpds. that modulate its activity.

SQ Sequence 502 AA;

Query Match 99.8%; Score 2698; DB 18; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1  MRCSFGVWLAALASLLHVSLSQGEFQRLKYKELVKNYNPLRPVANDSQPLTVVPSLSLL 60
QY      61  QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db      61  QIMDVDEKNQVLTNNIWLQMSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
QY      121  RFDATEHTNNVLNVSNGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWSLDL 180
Db      121  RFDATEHTNNVLNVSNGHCQVLPGLFKSSCYIDVRWPFDDVOHCKLFGSWSYGGWSLDL 180
QY      181  QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVDTFTVMRRRTLYYGLNLLIP 240
Db      181  QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVDTFTVMRRRTLYYGLNLLIP 240
QY      241  CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db      241  CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY      301  MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
Db      301  MIIVGLSVVTVIVLQYHHDDPGGKMPKWTTRVILLNCAWFLRMKRPGEKVRPACQHK 360
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Db      361  QRRCSLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDSGVVCGRWACSPTHDEHL 420
QY      421  LHGGQPEGPDLLAKILLEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db      421  LHGGQPEGPDLLAKILLEEVRYIANFRQCDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
QY      481  ICTIGILMSAPNFVEAVSKDFA 502
Db      481  ICTIGILMSAPNFVEAVSKDFA 502

```

RESULT 4

AAW09025

ID AAB24088 standard; Protein; 502 AA.

XX AAB24088;

XX 29-JAN-2001 (first entry)

XX Human PRO2145 protein sequence SEQ ID NO:77.

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumorigenesis; identification; cancer; cytostatic;
XX neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
XX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
XX neuronal disorder; gliai disorder; astrocytal disorder; angiogenic;
XX hypothalamic disorder; glandular disorder; macrophagal disorder;
XX epithelial disorder; stromal disorder; blastocoeleic disorder;
XX inflammatory disorder; immunologic disorder.

XX Homo sapiens.

XX WO200053755-A2.

XX

CC The present sequence is that of the alpha subunit of human
CC nicotinic acetylcholine receptor (nAChR). The sequence includes
CC regions that are conserved throughout the various nAChR alpha
CC subunits and which are essential for ligand binding. The invention
CC relates to water-soluble ligand-binding proteins derived from
CC molluscs, especially acetylcholine-binding proteins (AChBPs) and
CC analogues of ligand-gated ion channels, their crystals, and their
CC use for screening ligands of ligand-gated ion channels. The
CC water-soluble ligand-binding proteins are capable of forming
CC multimers and are amenable to crystallization. The crystal
CC structure of AChBP is provided, and can be used to generate 3D
CC models of the extracellular ligand-binding domain of ligand-gated
CC ion channels and thus for screening of drugs that act on these
CC ion channels. Chimeric proteins are provided that are capable of
CC binding a ligand of a ligand-gated receptor, and comprise at
CC least the amino acids of the AChBP determining solubility of the
CC AChBP, in the same positions as in the AChBP, and also comprising
CC amino acids determining binding to the ligand. In the chimeric
CC proteins, at least the essential amino acids of at least 1 of the
CC conserved regions of an nAChR have been substituted for the
CC corresponding amino acids, and preferably entire stretches have
CC been substituted. New drugs can be developed that selectively
CC intervene in neuronal signalling pathways, especially where the
CC ligand-gated ion channel is the nAChR, and the related disorder is
CC Tourette's syndrome, Alzheimer's disease, addiction to nicotine
CC or schizophrenia.
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 22; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLL 60
Db 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLL 60
QY 61 QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDILLYNSADE 120
QY 121 RFDATEFTNNLVNSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGSLDL 180
Db 121 RFDATEFTNNLVNSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTMMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTMMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPEGDPDLAKILEEVRYIANRFRQDESEAVCSWKFAACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFEAVSKDFA 502
Db 481 ICTIGILMSAPNFEAVSKDFA 502
RESULT 6
ID AAB50012
AAB50012 standard; Protein; 502 AA.

XX AAB50012;
AC 14-MAR-2001 (first entry)
DT
XX Wild-type human alpha7 ligand gated ion channel.
DE Human; alpha7 nicotinic acetylcholine gated ion channel;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
XX Homo sapiens.
OS
PN WO2000073431-A2.
XX
PD 07-DEC-2000.
PF
XX 25-MAY-2000; 2000WO-US11862.
PR
XX 27-MAY-1999; 99US-0136174.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
PI WPI; 2001-061524/07.
XX N-ESDB; AAC90380.
DR
XX
PT Special cell culture medium for treating cells and for inducing
PT mammalian cell lines to conduct calcium ions, comprising specified
PT concentrations of ions of sodium, calcium and potassium at specified pH
XX
PS Disclosure; Pages 61-63; 77pp; English.
CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the
CC cells.
XX
SQ Sequence 502 AA;
Query Match 99.8%; Score 2698; DB 22; Length 502;
Best Local Similarity 99.8%; Pred. No. 5.2e-260;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLL 60
Db 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKYNVNPPLRPVANDSQPLTVVFSLL 60
QY 61 QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNNIWLQMSWTDHYLQWNVSEYPGVKTFRFPDQGIWKPDILLYNSADE 120
QY 121 RFDATEFTNNLVNSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGSLDL 180
Db 121 RFDATEFTNNLVNSSGHCQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFSGWSYGGSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTMMRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEPYDPVTFVTMMRRRTLYYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCWFLRMKPGEDKVRPAQCHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

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Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGQVWCGMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
ID AAB50015 standard; Protein; 502 AA.
XX AAB50015;
AC AAB50015;
DT 14-MAR-2001 (first entry)
DE Mutant human alpha7 ligand gated ion channel #1.
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 230
FT /note= "Wild-type Thr substituted by Pro"
XX WO200073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US11862.
XX 27-MAY-1999; 99US-0136174.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90385.
XX Special cell culture medium for treating cells and for inducing
XX mammalian cell lines to conduct calcium ions, comprising specified
XX concentrations of ions of sodium, calcium and potassium at specified pH
XX
XX Claim 100; Pages 70-72; 77pp; English.
XX
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
XX gated ion channel. The human alpha7 ion channel was used in the
XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
XX ion channel can be expressed by recombinant cells in the present
XX invention, resulting in preferential calcium ion conductance by the
XX cells.
XX
XX Sequence 502 AA;
XX
Query Match 99.6%; Score 2692; DB 22; Length 502;
Best Local Similarity 99.6%; Pred. No. 2e-259;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MRCSPGVWJALAAASLLHVSILQGFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
Db 1 MRCSPGVWJALAAASLLHVSILQGFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSL 60
Qy 61 QINDVDEKNQVLTNWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120

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Db 61 QINDVDEKNQVLTNWLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDATHTNVLNVSNGHCQYLPGIPKSCYIDVRWFFPDVQHCCKLFGSWSYGGWSL 180
Db 121 RFDATHTNVLNVSNGHCQYLPGIPKSCYIDVRWFFPDVQHCCKLFGSWSYGGWSL 180
Qy 181 QMOEADISGYPNGEWDLVGIPIKRSERFYECCKEPEYPDVTFTVTRRRRLTYGLNLLIP 240
Db 181 QMOEADISGYPNGEWDLVGIPIKRSERFYECCKEPEYPDVTFTVTRRRRLTYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYF 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYF 300
Qy 301 MIIIVGLSVVTVIVLOVHHDDPGGKMPKTRVILLNKCWFLRMKPEGDKVRPACQHK 360
Db 301 MIIIVGLSVVTVIVLOVHHDDPGGKMPKTRVILLNKCWFLRMKPEGDKVRPACQHK 360
Qy 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGQVWCGMACSPTHDEHL 420
Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLDGVHCVPTPDGQVWCGMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRQDSEAVCSEWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 8
ID AAB50016 standard; Protein; 502 AA.
XX AAB50016;
AC AAB50016;
DT 14-MAR-2001 (first entry)
DE Mutant human alpha7 ligand gated ion channel #2.
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 241
FT /note= "Wild-type Cys substituted by Ser"
XX WO200073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US11862.
XX 27-MAY-1999; 99US-0136174.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90386.
XX Special cell culture medium for treating cells and for inducing
XX mammalian cell lines to conduct calcium ions, comprising specified
XX concentrations of ions of sodium, calcium and potassium at specified pH
XX
XX Claim 102; Pages 72-74; 77pp; English.

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XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the
CC cells.

XX SQ Sequence 502 AA;

Query Match 99.4%; Score 2688; DB 22; Length 502;
Best Local Similarity 99.6%; Pred. No. 5.1e-259;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
DB 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60

QY 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120

QY 121 RPDATFTNTLVNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCKLFGSWSGWSL 180
DB 121 RPDATFTNTLVNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCKLFGSWSGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 SVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480

RESULT 9
AAB50017
ID AAB50017 standard; Protein; 502 AA.
AC AAB50017;
XX 14-MAR-2001 (first entry)
DE Mutant human alpha7 ligand gated ion channel #3.
XX Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 230
FT /note= "Wild-type Thr substituted by Pro"
FT Misc-difference 241
FT /note= "Wild-type Cys substituted by Ser"

XX WO2000073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US11862.
XX 27-MAY-1999; 99US-0136174.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
XX WPI; 2001-061524/07.
XX N-PSDB; AAC90387.
XX Special cell culture medium for treating cells and for inducing
XX mammalian cell lines to conduct calcium ions, comprising specified
XX concentrations of ions of sodium, calcium and potassium at specified pH
XX
XX Claim 104; Pages 75-77; 77pp; English.
XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
XX gated ion channel. The human alpha7 ion channel was used in the
XX construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
XX gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
XX ion channel can be expressed by recombinant cells in the present
XX invention, resulting in preferential calcium ion conductance by the
XX cells.

XX SQ Sequence 502 AA;

Query Match 99.2%; Score 2682; DB 22; Length 502;
Best Local Similarity 99.4%; Pred. No. 2e-258;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60
DB 1 MRCSGGVWLAALASLLHVSLOGEFQRLKYLKELVKNYNPLRPVANDSQPLTVVFSLSLL 60

QY 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
DB 61 QIMDVDEKNQVLTNTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120

QY 121 RPDATFTNTLVNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCKLFGSWSGWSL 180
DB 121 RPDATFTNTLVNNSGHCQYLPGIFKSSCYIDVRWEPFDVQHCKLFGSWSGWSL 180

QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRTLYYGLNLLIP 240

QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 SVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300

QY 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
DB 301 MIIVGLSVVTVTVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360

QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

QY 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPPEGDPDLAKILEEVRYIANFRFCQDESEAVCSEWKFAACVVDRLCLMAFSVFTI 480

QY 481 ICTIGILMSAPNFVEAVSKDFA 502
DB 481 ICTIGILMSAPNFVEAVSKDFA 502

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RESULT 10
AAW12368
ID AAW12368 standard; Protein; 502 AA.
XX
AC AAW12368;
XX
DT 17-JUN-1997 (first entry)
XX
DE Neuronal alpha-bungarotoxin binding protein alpha1 subunit.
XX
KW Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
KW ligand binding; ion channel.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= Sig_peptide
FT /label= Mat_protein
XX
PN US5599709-A.
XX
PD 04-FEB-1997.
XX
PF 28-SEP-1989; 89US-0413947.
XX
PR 28-SEP-1989; 89US-0413947.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lindstrom JM, Schoepfer RD;
XX
DR WPI; 1997-118297/11.
DR N-PSDB; AAT59196.
XX
PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
PT to screen cholinergic agents and other drugs which may affect ligand
PT binding, ion channel or other activities of the protein.
XX
PS Example; Fig 2A-B; 18pp; English.
XX
CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
CC sequences of chick neuronal alpha-bungarotoxin binding protein
CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
CC obt'd. from an 18-day chick embryo cDNA library. ABBP subunits can
CC be produced in recombinant host cells, pref. a bacterium, and used
CC in the screening of cholinergic agents and other drugs that may
CC affect the ligand binding, ion channel or other activity of intact
CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
CC used to produce subunit peptides for use as immunogens for
CC preparing antibodies to permit affinity purification of subtypes
CC and their histological location.
XX
SQ Sequence 502 AA;

Query Match 89.9%; Score 2429; DB 18; Length 502;
Best Local Similarity 90.7%; Pred. No. 3.5e-233;
Matches 449; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 8 VMLAALASLHVSLOGEFQRLKYLKLVNPNPLRPVANDSQPLTVFSLQIMDYDE 67
DB 8 LWLLAAAGLVRESLQGSFQRLKYLKLVNPNPLRPVANDSQPLTVFSLQIMDYDE 67
QY 68 KNOVLTNIWLQSWTDHYLQWNVSEYPGVKTVRFPDGOIKWPKILLVNSADERDATHF 127
DB 68 KNOVLTNIWLQWWTWTHYLOWNVSEYPGVKTVRFPDGLIWKPKILLVNSADERDATHF 127
QY 128 TNVLNSSGHCQYLPPGIFKSSCYIDVRWPFDPVQHKLKFSGWSYGGWSDLQMQEADI 187
DB 128 TNVLNSSGHCQYLPPGIFKSSCYIDVRWPFDPVQKCNLKFSGWSYGGWSDLQMQEADI 187

188 SGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRTLYYGNLLIPCVLISAL 247
188 SGYISNGEWDLVGIPGKRSEFYECCKEYPDVTFTVTRRTLYYGNLLIPCVLISAL 247
248 ALLVFLLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDVPLIAQYFASTMIIVGLS 307
248 ALLVFLLPADSGEKISLIGITVLLSLTTFMLVAEIMPATSDVPLIAQYFASTMIIVGLS 307
308 VVTVTVIQLYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQKQRCSLA 367
308 VVTVTVIQLYHHHPDGGKMPKTRVILLNWCAMFLRMKRPGEKVRPACQKQRCSLS 367
368 SVENSAPPASNGNLLYIGFRLDGVHCVPDPDSGVVCGRMACSPHDEHLLHGGOPP 427
368 SMEMTVSGQCSNGNMLYIGFRLDGVHCPTPTTDSGVICGRMTCSPTTEENLLSHGHP 427
428 EGGDPLAKILLEEVRYIANRFRCODESEAVCSSEKFAACVVDRLCLMAFSVFTIICIGIL 487
428 EGGDPLAKILLEEVRYIANRFRDQDEEAICNEWKFAASVVDRLCLMAFSVFTIICIGIL 487
488 MSAPNFVEAVSKDFA 502
488 MSAPNFVEAVSKDFA 502

RESULT 11
AAW12369
ID AAW12369 standard; Protein; 511 AA.
XX
AC AAW12369;
XX
DT 17-JUN-1997 (first entry)
XX
DE Neuronal alpha-bungarotoxin binding protein alpha2 subunit.
XX
KW Neuronal alpha-bungarotoxin binding protein alpha 2; cholinergic;
KW ligand binding; ion channel.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= Sig_peptide
FT /label= Mat_protein
XX
PN US5599709-A.
XX
PD 04-FEB-1997.
XX
PF 28-SEP-1989; 89US-0413947.
XX
PR 28-SEP-1989; 89US-0413947.
XX
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Lindstrom JM, Schoepfer RD;
XX
DR WPI; 1997-118297/11.
DR N-PSDB; AAT59197.
XX
PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
PT to screen cholinergic agents and other drugs which may affect ligand
PT binding, ion channel or other activities of the protein.
XX
PS Example; Fig 3A-B; 18pp; English.
XX
CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
CC sequences of chick neuronal alpha-bungarotoxin binding protein
CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
CC obt'd. from an 18-day chick embryo cDNA library. ABBP subunits can
CC be produced in recombinant host cells, pref. a bacterium, and used
CC in the screening of cholinergic agents and other drugs that may

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CC affect the ligand binding, ion channel or other activity of intact
 CC ABPP subtypes. The ABPP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.
 XX
 SQ Sequence 511 AA;

Query Match 67.2%; Score 1816.5; DB 18; Length 511;
 Best Local Similarity 68.8%; Pred. No. 4.5e-172;
 Matches 342; Conservative 56; Mismatches 94; Indels 5; Gaps 4;
 QY 8 VMLAALASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLQLQMDVDE 67
 DB 16 LMASLFLSPFKVQQGSGQRRLYDLNRYNRLRPVNDSPQIVLQSLQLQMDVDE 75
 QY 68 KNOVLTTNIWLQMSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLVNSADERFATFH 127
 DB 76 KNOVLITNAWLQWVDIYLSWDQYEPGVQNLRFPSDQIWPDPILLVNSADERFATFH 135
 QY 128 TNLVNSSGHQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGWSLQDQOEADI 187
 DB 136 TNLVNVSGSQVIPPGLKSTCYIDVRWPFDFVQKCDLKFGSWTHSGWLDLQMLEADI 195
 QY 188 SGVYPNGEWDLVGIPGRSERFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISAL 247
 DB 196 SNYISNGEWDLVGVPGRKNLYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIPCVLISGL 255
 QY 248 ALLVFLPADSGKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASVMIIVGLS 307
 DB 256 ALLVFLPADSGKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFASVMIIVGLS 315
 QY 308 VVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRP-AQCHK--QRRC 364
 DB 316 VVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRP-AQCHK--QRRC 374
 QY 365 SLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPHDEHLLHG 424
 DB 375 SLKNTENVLPGHQPSNGNMIY-SYHTMENPCCPNNDLGSKSGKITCPLSEDNHVRQKK 433
 QY 425 QPEGPDPLAKILEEVRYIANRRCODESEAVCSEWKAACVVDRLCLMAFSVFTICTI 484
 DB 434 ALMDTTPVIVKILEEVQFIAMRFRKODEGEEICSEWKAFAAVIDRLCLVAFTLFAICTF 493
 QY 485 GILMSAPNFVAVSKDF 501
 DB 494 TILMSAPNFIEAVSKDF 510

RESULT 12
 AAB50014
 ID AAB50014 standard; Protein; 470 AA.
 XX
 AC AAB50014;

XX 14-MAR-2001 (first entry)

DE Chimeric alpha7/5-HT3 ligand gated ion channel.

XX Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX

OS Chimeric - Mus musculus.

OS Chimeric - Homo.sapiens.

XX WO2000073431-A2.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US11862.

XX 27-MAY-1999; 99US-0136174.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR N-PSDB; AAC90382.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 PS Claim 97; Pages 66-68; 77pp; English.
 XX
 CC The present sequence is a chimeric human alpha7 nicotinic
 CC acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand gated ion
 CC channel. The alpha7/5-HT3 chimeric ion channel can be expressed by
 CC recombinant cells in the present invention, resulting in preferential
 CC calcium ion conductance by the cells.
 XX

SQ Sequence 470 AA;

Query Match 54.6%; Score 1474.5; DB 22; Length 470;
 Best Local Similarity 58.7%; Pred. No. 5.2e-138;
 Matches 294; Conservative 46; Mismatches 94; Indels 67; Gaps 9;
 QY 1 MRCSPGGVWLALASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60
 DB 1 MRCSPGGVWLALASLLHVSLSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60
 QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLVNSADE 120
 DB 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLVNSADE 120
 QY 121 RFDATFTNLVNSSGHQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGWSL 180
 DB 121 RFDATFTNLVNSSGHQVLPFGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGRSERFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGRSERFYECCKEPEYDPDVTFTVMRRRTLYYGLNLLIP 239
 QY 241 CVLISALALLVFLPADSGEKISLIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAS 300
 DB 240 SIFLWVDIVGFCPLPDSGERVSFKITLLGYSVFLIIVSDTLPATI-GTPLIGYFVVC 298
 QY 301 MIIVGLSVVTVIVLQVHHDDPDGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 299 MALLVIVSLAETIFIVRLVHKODLQRPVDPDLRLHLVLDRIAIVLCL---GEQFM----- 348
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPHDEHL 420
 DB 349 -----AHRPPATFOAN-----KTDD-----CSGSLLPANGNHC 377
 QY 421 LHGG-----QPGEQPDOLA--KILEEVRYIANRRCODESEAVCSEWKA 463
 DB 378 SHVGGPDLEKTPRGSGPLPPPREASLAVRGLLQELSSIRHFLKRDREVARDLRLV 437
 QY 464 ACVVDR-----LCLMAFSV 477
 DB 438 GYVLDRLLFRIYLLAVLAYS 458

RESULT 13

AAB50018

ID AAB50018 standard; Protein; 448 AA.

XX AAB50018;

XX 14-MAR-2001 (first entry)

XX Mature cell surface chimeric alpha7/5-HT3 ligand gated ion channel.

KW Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX WO200073431-A2.
 PN
 XX 07-DEC-2000.
 XX
 XX 25-MAY-2000; 2000WO-US11862.
 XX
 XX 27-MAY-1999; 99US-0136174.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 XX WPI; 2001-061524/07.
 XX
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 XX Disclosure; Fig 2; 77pp; English.
 PS
 XX The present sequence is the mature cell surface form of a chimeric human
 CC alpha7 nicotinic acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand
 CC gated ion channel (the full protein sequence is given in AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells.
 XX
 XX Sequence 448 AA;
 SQ
 Query Match 50.3%; Score 1360.5; DB 22; Length 448;
 Best Local Similarity 56.8%; Pred. No. 1.1e-126;
 Matches 272; Conservative 46; Mismatches 94; Indels 67; Gaps 9;
 QY 23 GEFQRLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTTNIWLQSW 82
 Db 1 GEFQRLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKNOVLTTNIWLQSW 60
 QY 83 TDHYLQWNVSEYPCVKTVPDQGIWKPDILLYNSADERFDTHTNVLNSSGHCQYLP 142
 Db 61 TDHYLQWNVSEYPCVKTVPDQGIWKPDILLYNSADERFDTHTNVLNSSGHCQYLP 120
 QY 143 PGIFKSCYIDVRWFPDQVCHCKLKFGSWSGWSLQMOEADISGYIPNGEWDLVGIP 202
 Db 121 PGIFKSCYIDVRWFPDQVCHCKLKFGSWSGWSLQMOEADISGYIPNGEWDLVGIP 180
 QY 203 GKSERPYECKEYPDVTFTVMRRRLTYGMLNLLIPCVLISALALLVFLPADSGEKI 262
 Db 181 GKSERPYECKEYPDVTFTVMRRRLTYGMLNLLIPCVLISALALLVFLPADSGERV 239
 QY 263 SLGITVLLSITFTMLVAETMPATSDVPLIAQYFASFTMIIVGLSVVTVIVLQYHHDP 322
 Db 240 SFKITLLGYSVFLLIISDTLPATI-GTPLIGYFVVMALLVISLAETIFIVRLVHKQD 298
 QY 323 DGGKMPKWTIVILLNCAWFLMKRPGEDKVRPACQHKQRCRSLASVEMSAVAPPASNG 382
 Db 299 LQRPVDPWLHLVLDRIAAILCL--GEQPM-----AHRPPATPQA 336
 QY 383 NLLYIGFRGLDVHCVTPDPSGVVCGRMACSPTHDEHLLHGG-----QPP 427
 Db 337 N-----KTDD--CSGSDLLPAMGNHCHSVGGQDLEKTPRGRGSLPP 377
 QY 428 EGDPDLA--KILEVRVIANFRQDESEAVCSWKFACVVD--LCLMAFSV 477
 Db 378 PREASLAVRGLLOELSSIRHLEKRDREMRVARDWLVRGVYLDRLLFRIYLLAVLAYSI 436

RESULT 14
 AAY50816
 ID AAY50816 standard; Protein; 501 AA.
 XX
 AC AAY50816;
 XX
 DT 17-FEB-2000 (first entry)
 XX
 DE H. virescens acetyl-choline receptor protein from clone Hva7-2.
 XX
 KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; ACHR.
 XX
 OS Heliothis virescens.
 XX
 PN DE19819829-A1.
 XX
 PD 11-NOV-1999.
 XX
 XX 04-MAY-1998; 98DE-1019829.
 XX
 XX 04-MAY-1998; 98DE-1019829.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Adamczewski M, Oellers N, Schulte T;
 XX
 DR WPI; 2000-014207/02.
 DR N-PSDB; AAZ24477.
 XX
 XX New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides -
 XX
 XX Example 1a; Page 22-23; 26pp; German.
 XX
 CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of ACHR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related ACHR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from Heliothus virescens.
 XX
 SQ Sequence 501 AA;
 Query Match 46.4%; Score 1254.5; DB 21; Length 501;
 Best Local Similarity 48.4%; Pred. No. 5e-116;
 Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;
 QY 10 LALAASLIHVSLOQEFQKLYKLVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 Db 8 LALLA-LLPVSEQGPHEKRLNALLANNYTLERPVANSEPLEVRFGLTLOQIIDVDEKN 66
 QY 70 QVLTTNIWLQSWTDHYLQWNVSEYPCVKTVPDQGIWKPDILLYNSADERFDTHTN 129
 Db 67 QLLITNIWLSLEWYNDYLNWNSDEYGGVKDLRITPNKLVKPDVLMYNSADEGFDGTYQTN 126
 QY 130 VLVNSSGHCQYLPQIFKSCYIDVRWFPDQVCHCKLKFGSWSGWSLQMOE--AD 186
 Db 127 VVNRSGSCLVPPGIFKSTCKMDIAWFPDQDCHDKMFGSWTYDGNLDLVLDKDAAGD 186
 QY 187 ISGYIPNGEWDLVGIPGKRSEFYECKEYPDVTFTVMRRRLTYGMLNLLIPCVLISA 246
 Db 187 LSDFITNGEWYLGWPGKKNITITACCEPYVDVTFIMIRRLTYEFNLIIVPCVLIS 246
 QY 247 LALLVFLPADSGEKISGITVLLSITFTMLVAETMPATSDVPLIAQYFASFTMIIVGL 306
 Db 247 MALLGFTLPDPSGEEKITLGVITILLSLTVFLNLVAETLPOVSDAIPLLGTIFYNCIMFVAS 306

QY 4 SPGGWLAALASLLHVSLSQGEFQRKLYKELVKYNVNPLERPVPANDSQPLTYVFSLSLLOIM 63

D6 12 APAGLLLLLCLLWPGRCGCGYHEKRLHLLHLLDHYNVLEPVPVNESDPLOLSEGLTMOII 71

Search completed: June 20, 2003, 18:58:22
Job time : 76 secs

D**b**

Result No.	Score	Query %			ID	Description
		Match	Length	DB		
1	87	17.3	157	6	Q9TUL2	Q9Tul2 macaca mula
2	68	13.5	68	6	Q9TUC7	Q9Tuc7 macaca mula
3	62	12.4	502	11	Q9JHD6	Q9Jhd6 mus musculus
4	45	9.2	86	13	Q9OXF5	Q9Oxf5 cormix co
5	37	7.4	65	11	Q9EP09	Q9epu9 rattus norv
6	34	6.8	115	11	Q8V109	Q8v109 mus musculus
7	27	5.4	511	13	Q03481	Q03481 gallus gall
8	12	2.4	573	5	Q9GQU9	Q9gqu9 caenorhabdi
9	11	2.2	500	5	Q22224	Q22224 caenorhabdi
10	10	2.0	134	11	Q99MD4	Q99md4 meriones un
11	10	2.0	477	11	Q62959	Q62999 rattus norv
12	10	2.0	483	6	Q9N0F4	Q9nuf4 mustela put
13	10	2.0	484	4	Q9BS29	Q9bs29 homo sapien
14	10	2.0	484	11	Q70213	Q70213 cavia porce
15	10	2.0	490	11	Q70212	Q70212 cavia porce
16	10	2.0	510	4	Q60854	Q60854 homo sapien

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DB 131 RLCLMAFSVFTICTIGILMSAPNFV 157
|||||
RESULT 2
Q9TUC7 PRELIMINARY; PRT; 68 AA.
AC Q9TUC7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7 subunit (Fragment).
OS Macaca mulatta (Rhesus macaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekhon H.S., Jia Y., Raab R., Kuryatov A., Pankow J.F., Whitsett J.A.,
RA Lindstrom J., Spindel E.R.;
RT "prenatal nicotine exposure increases alpha 7 nicotinic acetylcholine
RT receptor expression in pulmonary cells and alters fetal lung
RT development in monkeys.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087689; AAF02221.1;
DR InterPro: IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 68 AA; 7700 MW; B18048F0948B6477 CRC64;
Query Match 13.5%; Score 68; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.5e-63;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 435 KILEEVYIANRRCQDESAVSEWKFACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
|||||
DB 1 KILEEVYIANRRCQDESAVSEWKFACVVDRLCLMAFSVFTICTIGILMSAPNFV 60
QY 495 EAVSKDFA 502
|||||
DB 61 EAVSKDFA 68
RESULT 3
Q9JHD6 PRELIMINARY; PRT; 502 AA.
AC Q9JHD6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha 7.
GN CHRNA7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21BG;
RX MEDLINE=97189245; PubMed=9037516;
RA Stitzel J.A., Farnham D.A., Collins A.C.;
RT "Linkage of strain-specific nicotinic receptor alpha 7 subunit
RT restriction fragment length polymorphisms with levels of alpha-
RT bungarotoxin binding in brain.";
RL Brain Res. Mol. Brain Res. 43:30-40 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/21BG;
RA Stitzel J.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1, SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC EMBL; AF225980; AAF35885.1; -.
DR MGD; MGI:99779; Chnra7.
DR InterPro: IPR000188; GABAA_receptor.
DR InterPro: IPR001175; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;
Query Match 12.4%; Score 62; DB 11; Length 502;
Best Local Similarity 100.0%; Pred. No. 9.3e-56;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 LYKELVKNYNPLERPANDSQPLTVYFSLSLQIMDVDEKQVLTNIWLQMSWDHYLQ 88
|||||
DB 29 LYKELVKNYNPLERPANDSQPLTVYFSLSLQIMDVDEKQVLTNIWLQMSWDHYLQ 88
QY 89 WN 90
|||
DB 89 WN 90
RESULT 4
Q90XF5 PRELIMINARY; PRT; 86 AA.
AC Q90XF5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha-7 chain
DE (Fragment).
OS Coturnix coturnix (common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP SEQUENCE FROM N.A.
RA Bader A.G., Schneider M.L., Bister K., Hartl M.;
RT "TO3, a target of the v-Jun transcription factor, encodes a protein
RT with transforming activity related to human microspherule protein 1
RT (MCRS1).";
RL Oncogene 0:0-0 (2001).
DR EMBL; AF390033; AAK73731.1; -.
DR InterPro: IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9700 MW; 445314D42B08E4CA CRC64;
Query Match 9.2%; Score 46; DB 13; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.1e-39;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 321 DPGGKMPKWTFRVILLNCAMFLRMKRPGEKVRPACQHKQRCSL 366
|||||
DB 1 DPGGKMPKWTFRVILLNCAMFLRMKRPGEKVRPACQHKQRCSL 46
RESULT 5
Q9EPU9 PRELIMINARY; PRT; 65 AA.
AC Q9EPU9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic receptor alpha 7 subunit (Fragment).
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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=21264418; PubMed=11278551;
RA Nagavara U., Danthi S., Boyd R.T.;
RT "Characterization of a Rat Neuronal Nicotinic Acetylcholine Receptor
  alpha 7 Promoter.";
RL J. Biol. Chem. 276:16749-16757 (2001).
DR EMBL; AF321242; AAG39219.1; -.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
KW Receptor.
FT NON_TER
FT SEQUENCE 65 65
SQ SEQUENCE 65 AA; 7305 MW; 7C795E602A0CA2AB CRC64;

Query Match 7.4%; Score 37; DB 11; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.2e-30;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LYKELVKNPLRPVANDSQPLTVVFSLSLQIMDV 65
DB 29 LYKELVKNPLRPVANDSQPLTVVFSLSLQIMDV 65
|||||
RESULT 6
OBVIO9 PRELIMINARY; PRT; 115 AA.
ID Q8V109
AC Q8V109;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 7 subunit (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kuo Y.-P., Lukas R.J.;
RT "Expression of mouse nicotinic acetylcholine receptor genes in the
  developing thymus.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325348; AAL37364.1; -.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
KW Receptor.
FT NON_TER
FT SEQUENCE 115 115
SQ SEQUENCE 115 AA; 13586 MW; 45D637A1FF6E7CA7 CRC64;

Query Match 6.8%; Score 34; DB 11; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.9e-27;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 VRFPDQIQWPKDILLVNSADRFDAFTHTNLVYN 133
DB 49 VRFPDQIQWPKDILLVNSADRFDAFTHTNLVYN 82
|||||
RESULT 7
Q03481 PRELIMINARY; PRT; 511 AA.
ID Q03481
AC Q03481;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=90311518; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RT "Brain alpha-bungarotoxin-binding protein cDNAs and mABs reveal
  subtypes of this branch of the ligand-gated ion channel gene
  superfamily.";
RL Neuron 5:35-48 (1990).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; X52296; CAA36544.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
  Transmembrane.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 511 POTENTIAL.
FT SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;

Query Match 5.4%; Score 27; DB 13; Length 511;
Best Local Similarity 100.0%; Pred. No. 3.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 LALLVFLPADSGEKISLGITVLLSLT 273
DB 255 LALLVFLPADSGEKISLGITVLLSLT 281
|||||
RESULT 8
Q9GQU9 PRELIMINARY; PRT; 573 AA.
ID Q9GQU9
AC Q9GQU9; Q21615;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor-like subunit ACR-12 (R01E6.4
  protein).
DE R01E6.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RX MEDLINE=92200102; PubMed=10100329;
RA Morgan N.P., Baylis H.A., Adcock C., Smith G.R., Sansom M.S.,
  Sattelle D.B.;
RT "An extensive and diverse gene family of nicotinic acetylcholine
  receptor alpha subunits in Caenorhabditis elegans.";
RL Recept. Channels 6:213-228 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Morgan N.P., Gower N.J.D., Culetto E., Sattelle D.B.;
RT "Isolation and characterization of two novel nicotinic acetylcholine
  receptor alpha subunit encoding cDNAs from the nematode,
  Caenorhabditis elegans.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

```

RA Coles L.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AF187013; AAG35183.1; -.
DR EMBL; Z68118; CAA92184.2; -.
DR InterPro; IPR001188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
Transmembrane.
SQ SEQUENCE 573 AA; 65707 MW; 5CFBACF3903548B2 CRC64;

Query Match 2.4%; Score 12; DB 5; Length 573;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 DVDEKNQVLTTN 75
| | | | | | | | | |
DB 76 DVDEKNQVLTTN 87

RESULT 9

Q22224 ID Q22224 PRELIMINARY; PRT; 500 AA.
AC Q22224;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE T05C12.2 protein.
GN T05C12.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Burton J.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; Z66500; CAA91304.2; -.
DR InterPro; IPR002106; AATRNA_ligaseII.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 500 AA; 57675 MW; 20BD4CBF19614892 CRC64;

Query Match 2.2%; Score 11; DB 5; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61 QIMDVDEKNQV 71
| | | | | | | | | |
DB 56 QIMDVDEKNQV 66

RESULT 10

Q99MD4 ID Q99MD4 PRELIMINARY; PRT; 134 AA.
AC Q99MD4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acetylcholine receptor alpha 9 subunit (Fragment).
GN NACHR.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RA He D.Z., Zheng J., Dallos P.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350252; AAK29438.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR Pfam; PF02932; Neur_chan_memb; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 134 134
SQ SEQUENCE 134 AA; 14779 MW; 74925CD3D70C8999 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 NLLIPCVLIS 245
| | | | | | | | | |
DB 5 NLLIPCVLIS 14

RESULT 11

Q62999 ID Q62999 PRELIMINARY; PRT; 477 AA.
AC Q62999;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE SHT3 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson D.S.;
RL "Rat SHT3 receptor sequence."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; U59672; AAB02949.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_chan_LBD; 1.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
Transmembrane.
SQ SEQUENCE 477 AA; 54837 MW; 3DCCFC34F175FCC3 CRC64;

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Query Match      2.0%; Score 10; DB 11; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 65 VDEKNQVLTT 74
   |||||
Db 72 VDEKNQVLTT 81

RESULT 12
ID Q9N0F4 PRELIMINARY; PRT; 483 AA.
AC Q9N0F4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ferret 5-HT3A receptor.
OS Mustela putorius furo (Ferret).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9669;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RX MEDLINE=20344772; PubMed=10884508;
RA Mochizuki S., Watanabe T., Miyake A., Saito M., Furuichi K.;
RT "Cloning, expression, and characterization of ferret 5-HT3 receptor
RT subunit";
RL Eur. J. Pharmacol. 399:97-106(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AB029898; BAA96417.1; -.
DR InterPro; IPR000188; GABAA receptor.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 483 AA; 55562 MW; 54695AC794E30206 CRC64;

Query Match      2.0%; Score 10; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 65 VDEKNQVLTT 74
   |||||
Db 78 VDEKNQVLTT 87

RESULT 13
ID Q9BSZ9 PRELIMINARY; PRT; 484 AA.
AC Q9BSZ9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 55.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; BC004453; AAH04453.1; -.

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DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001005; Myb_DNA_binding.
DR InterPro; IPR001175; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00334; MYB 2; UNKNOWN 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Hypothetical protein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 484 AA; 55894 MW; 74F70567007BCB51 CRC64;

Query Match      2.0%; Score 10; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
   |||||
Db 79 VDEKNQVLTT 88

RESULT 14
ID O70213 PRELIMINARY; PRT; 484 AA.
AC O70213
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 5-HT3-As receptor precursor.
GN 5-HT3.
OS Cavia porcellus (Guinea pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RX MEDLINE=98130690; PubMed=9463477;
RA Laukiewicz S., Lobitz N., Wetzel C.H.R., Rupprecht R., Gisselmann G.,
RA Hatt H.;
RT "Molecular cloning, functional expression, and pharmacological
RT characterization of 5-hydroxytryptamine3 receptor cDNA and its splice
RT variants from guinea pig.";
RL Mol. Pharmacol. 53:202-212(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; AF006462; AAC06137.1; -.
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur_Channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 484 5-HT3-AS RECEPTOR.
SQ SEQUENCE 484 AA; 55087 MW; F7CF69D582ADBC82 CRC64;

Query Match      2.0%; Score 10; DB 11; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
   |||||
Db 78 VDEKNQVLTT 87

RESULT 15
ID O70212 PRELIMINARY; PRT; 490 AA.

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AC 070212;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 5-HT3-A1 receptor precursor.
 GN 5-HT3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]__
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE=98130690; PubMed=9463477;
 RA Lankiewicz S., Lobitz N., Wetzel C.H.R., Rupprecht R., Gisselmann G.,
 RA Hatt H.;
 RT "Molecular cloning, functional expression, and pharmacological
 RT characterization of 5-hydroxytryptamine₁ receptor cDNA and its splice
 RT variants from guinea pig.";
 RL Mol. Pharmacol. 53:202-212(1998).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR EMBL: AF006461; AAC06136.1; -.
 DR InterPro; IPR000188; GABAA_receptor.
 DR InterPro; IPR001175; Neur_Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRPFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 490 5-HT3-AL RECEPTOR.
 SQ SEQUENCE 490 AA; 53655 MW; EDB32F8597494F61 CRC64;

Query Match 2.0%; Score 10; DB 11; Length 490;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87

Search completed: June 20, 2003, 19:13:42
 Job time : 88 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:01:56 ; Search time 24 Seconds
(without alignments)
867.547 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGWLLAASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 112892 seqs, 41476328 residues
Word size : 6

Total number of hits satisfying chosen parameters: 996

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	79.9	502	1 ACH7 HUMAN	P36544 homo sapien
2	92	18.3	502	1 ACH7 CHICK	P22770 gallus gall
3	71	14.1	499	1 ACH7 BOVIN	P54131 bos taurus
4	62	12.4	502	1 ACH7 MOUSE	P49582 mus musculus
5	62	12.4	502	1 ACH7 RAT	O05941 rattus norv
6	10	2.0	478	1 SHT3 HUMAN	P46098 homo sapien
7	10	2.0	479	1 ACH9 HUMAN	Q9ugml homo sapien
8	10	2.0	479	1 ACH9 RAT	P43144 rattus norv
9	10	2.0	483	1 SHT3 RAT	P35563 rattus norv
10	10	2.0	487	1 SHT3 MOUSE	P23979 mus musculus
11	9	1.8	436	1 ACHX ONCVO	P54247 onchocerca
12	9	1.8	450	1 ACHX HUMAN	Q9g226 homo sapien
13	9	1.8	498	1 ACHX CAEEL	P48180 caenorhabdi
14	9	1.8	511	1 ACH5 CAEEL	Q23022 caenorhabdi
15	9	1.8	557	1 ACH1 SCHGR	P23414 schistocerc
16	9	1.8	576	1 ACH2 DROME	P17644 drosophila
17	8	1.6	496	1 ACH3 CHICK	P09481 gallus gall
18	8	1.6	513	1 ACHD CHICK	P02717 gallus gall
19	8	1.6	517	1 ACHD HUMAN	Q07001 homo sapien
20	8	1.6	521	1 ACHD XENLA	P09628 xenopus lae
21	8	1.6	567	1 ACH1 DROME	P09478 drosophila
22	8	1.6	1072	1 ITA6 CHICK	P26007 gallus gall
23	8	1.6	1091	1 ITA6 MOUSE	Q61739 mus musculus
24	7	1.4	67	1 HMT2 METHH	Q27731 methanobact
25	7	1.4	69	1 HMT2 METHF	P19267 methanobact
26	7	1.4	127	1 RPOZ RICCN	Q92h89 rickettsia
27	7	1.4	144	1 PSB1 ECOLI	P10031 escherichia
28	7	1.4	144	1 PSB2 ECOLI	P10032 escherichia
29	7	1.4	174	1 CSF3 SHEEP	Q28746 ovis aries
30	7	1.4	175	1 HES3 RAT	Q04667 rattus norv
31	7	1.4	195	1 CSF3 BOVIN	P35833 bos taurus
32	7	1.4	195	1 CSF3 FIG	O02837 sus scrofa
33	7	1.4	198	1 SCP2 BACSU	P81100 bacillus su

ALIGNMENTS

RESULT 1

ACH7_HUMAN	7	1..4	216	1	ATP6_AQUAE	066566	aquifex aso					
AC	35	7	230	1	FLAH_METVO	O06641	mechanococc					
DT	36	7	262	1	ZNOB_BUCAL	P57402	buchnera ap					
DT	37	7	269	1	Y32B_MYCGE	Q92b74	mycoplasma					
DT	38	7	290	1	LEP_HELPJ	Q92lq5	helicobacte					
DT	39	7	290	1	LEP_HELPJ	O25300	helicobacte					
DT	40	7	316	1	Y273_SYNY3	P73894	synecocyst					
DT	41	7	321	1	SAPB_SALTY	P36668	salmonella					
DT	42	7	347	1	NU2M_RHIUN	Q96061	rhinoceros					
DT	43	7	353	1	BRB1_HUMAN	P46663	homo sapien					
DT	44	7	376	1	DXR_TREPA	O83610	treponema p					
DT	45	7	398	1	YJ16_CAUCR	Q9a710	caulobacter					
STANDARD; PRT; 502 AA.												
ACH7_HUMAN	AC	P36544; Q15826; Q99555; Q96RH2; Q9BXH0;										
DT	01-JUN-1994	(Rel. 29, Created)										
DT	01-NOV-1997	(Rel. 35, Last sequence update)										
DT	15-JUN-2002	(Rel. 41, Last annotation update)										
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.											
GN	CHRNA7 OR NACHRA7.											
OS	Homo sapiens (Human).											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
OX	NCBI_TaxID=9606;											
RN	(1)											
RP	SEQUENCE FROM N.A.											
RC	TISSUE=Brain;											
RX	MEDLINE=94195283; PubMed=8145738;											
RA	Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;											
RT	"Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes.";											
RT	Mol. Pharmacol. 45:546-554(1994).											
RL	(2)											
RN	SEQUENCE FROM N.A.											
RP	TISSUE=Hippocampus;											
RA	Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;											
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.											
RP	(3)											
RN	SEQUENCE FROM N.A.											
RP	MEDLINE=97062879; PubMed=8906617;											
RA	Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,											
RA	Chavez-Noriega L.E., Johnson E.C., Vellicolebi G., Harpold M.M.;											
RT	"Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.";											
RT	J. Mol. Neurosci. 7:217-228(1996).											
RL	(4)											
RN	SEQUENCE FROM N.A.											
RP	MEDLINE=97162233; PubMed=9009220;											
RA	Groot Kormelink P.J., Luyten W.H.M.L.;											
RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal Nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.";											
RT	FEBS Lett. 400:309-314(1997).											
RL	(5)											
RN	SEQUENCE FROM N.A.											
RP	TISSUE=Epidermal keratinocytes;											
RA	Arredondo J., Grando S.A.;											
RT	"Cloning cholinergic receptors in human keratinocytes.";											

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

[7]
RN SEQUENCE OF 17-502 FROM N.A.
RP
RC TISSUE=Brain;
RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
RA Lee J., Tian J., Giordano T.;
RT "Cloning and sequence of the human a7 nicotinic acetylcholine
RT receptor.";
RL Drug Dev. Res. 30:252-256(1993).
RN [8]
RN SEQUENCE OF 24-502 FROM N.A.
RP
RC TISSUE=Retina;
RX MEDLINE=94245214; PubMed=8188270;
RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
RA Heinemann S.F.;
RT "Molecular cloning and chromosomal localization of the human alpha 7-
RT nicotinic receptor subunit gene (CHRNA7).";
RL Genomics 19:379-381(1994).
RN [9]
RN SEQUENCE OF 118-129 FROM N.A.
RP
RC PubMed=11829490;
RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
RX "A 3-Mb map of a large segmental duplication overlapping the alpha7-
RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
RL Genomics 79:197-209(2002).
RN [10]
RN MASS SPECTROMETRY.
RP
RC TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC
CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -1- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI..
CC
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC tion between the Swiss Institute of Bioinformatics and the EMBL outstat-
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CC cial entities requires a license agreement (See <http://www.isb-sib.ch/anno>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC ENBL; X70297; CAA49778.1; -
CC DR ENBL; U40583; AAA83561.1; -
CC DR ENBL; U62436; AAB40114.1; -
CC DR ENBL; Y08420; CAA69697.1; -
CC DR ENBL; AF385585; AAK68111.1; -
CC DR ENBL; L25827; -; NOT_ANNOTATED_CDS.
CC DR ENBL; L23141; CAA80672.1; -
CC DR ENBL; AF332758; AAK19515.1; -
CC DR Genew; HGNC:1960; CHRNA7.
CC MIM; 118511; -
CC InterPro; IPR000188; GABAA_receptor.
CC DR InterPro; IPR001175; Neur_channel.
CC DR Pfam; PF02931; Neur_chan_LBD; 1.
CC DR Pfam; PF02932; Neur_chan_memb; 1.
CC DR PRINTS; PR00252; NRIONCHANNEL.
CC DR TIGRFAMS; TIGR00860; IIC; 1
CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC DR Postsynaptic membrane, Ionic channel; Glycoprotein; Signal;
CC Transmembrane; Multigene family
KW

FT	SIGNAL	1	22	BY SIMILARITY.
FT	CHAIN	23	502	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN.
FT	DOMAIN	23	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	255	POTENTIAL.
FT	TRANSMEM	262	280	POTENTIAL.
FT	TRANSMEM	296	317	POTENTIAL.
FT	DOMAIN	318	469	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	470	490	POTENTIAL.
FT	DISULFID	150	164	BY SIMILARITY.
FT	DISULFID	212	213	ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	11	11	A -> G (IN REF. 1 AND 7).
FT	CONFLICT	58	58	S -> N (IN REF. 2 AND 6).
FT	CONFLICT	134	134	S -> P (IN REF. 2 AND 6).
FT	CONFLICT	364	364	C -> S (IN REF. 8).
FT	CONFLICT	375	375	A -> G (IN REF. 1).
FT	CONFLICT	409	413	RMACS -> AWPAP (IN REF. 8).
FT	CONFLICT	409	413	RMACS -> AWPAP (IN REF. 8).
FT	SEQUENCE	502 AA;	56449 MW;	D94B3A482EAA0E42 CRC64;
Query Match			79.9%;	Score 401; DB 1; Length 502;
Best Local Similarity			99.8%;	Pred. No. 0;
Matches 501; Conservative			0;	Mismatches 1; Indels 0; Gaps 0;
Qy	1	MRCSPGSGVWLAALASLLHVS	LQSGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL	60
Db	1	MRCSPGSGVWLAALASLLHVS	LQSGEFQRKLYKELVKNYNPLRPVANDSQPLTVYFSL	60
Qy	61	QIMDVDEKNOVLTTNIWLQMS	TDHTYQLQNVSEYPGVKTVRFPDQGIWKPDILLYNSADE	120
Db	61	QIMDVDEKNOVLTTNIWLQMS	TDHTYQLQNVSEYPGVKTVRFPDQGIWKPDILLYNSADE	120
Qy	121	RFDATEFTNVLNSSGHCQYL	PPGIFKSSCYIDVRWPFDPVQHCKLFGSGWSYCGWSL	180
Db	121	RFDATEFTNVLNSSGHCQYL	PPGIFKSSCYIDVRWPFDPVQHCKLFGSGWSYCGWSL	180
Qy	181	QMOEADISGYIPNGEWDLV	GIPIGKRSEFYECCKEYPDVDTFTVTMRRTLYYGLNLLIP	240
Db	181	QMOEADISGYIPNGEWDLV	GIPIGKRSEFYECCKEYPDVDTFTVTMRRTLYYGLNLLIP	240
Qy	241	CVLISALALVFLPADSGEK	ISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Db	241	CVLISALALVFLPADSGEK	ISIGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST	300
Qy	301	MIIVGLSVVTVIVLQYHH	DDPGGKMPKXTRVILLNWCANFLRMKRPGEKVRPACQHK	360
Db	301	MIIVGLSVVTVIVLQYHH	DDPGGKMPKXTRVILLNWCANFLRMKRPGEKVRPACQHK	360
Qy	361	QRCSSLASVMSAVAPPAS	NGNLLYIGFRLDGVCHVCTPDSDGVVCGRMACSPTHDEHL	420
Db	361	QRCSSLASVMSAVAPPAS	NGNLLYIGFRLDGVCHVCTPDSDGVVCGRMACSPTHDEHL	420
Qy	421	LHGQOPPEGDPDLAKIL	EEVRYIANRFRCDSEAVCSEWKFAACVDRCLCLMAFSVTI	480
Db	421	LHGQOPPEGDPDLAKIL	EEVRYIANRFRCDSEAVCSEWKFAACVDRCLCLMAFSVTI	480
Qy	481	ICTIGILMSAPNFVEAVS	KOFA 502	
Db	481	ICTIGILMSAPNFVEAVS	KOFA 502	
RESULT 2				
ACH7 CHICK				
ID	ACH7 CHICK	STANDARD;	PRT;	502 AA.
AC	P22770;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
OS	Gallus gallus (Chicken).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91097796; PubMed=1702646;
 RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
 Millar N., Valera S., Barkas T., Ballivet M.;
 RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
 RT developmentally regulated and forms a homo-oligomeric channel blocked
 RT by alpha-BTX.";
 RL Neuron 5:847-856 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=90315158; PubMed=2369519;
 RA Schoepfer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
 RT "Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal
 RT subtypes of this branch of the ligand-gated ion channel gene
 RT superfamily.";
 RL Neuron 5:35-48 (1990).
 RN [3]
 RP SEQUENCE OF 1-18 FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Erythrocyte;
 RX MEDLINE=93049204; PubMed=1425587;
 RA Matter-Sadzinski L., Hernandez M.C., Rottocil T., Ballivet M.,
 Matter J.M.;
 RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
 RT promoter develops during morphogenesis of the central nervous
 RT system.";
 RL EMBO J. 11:4529-4538 (1992).
 RN [4]
 RP SEQUENCE OF 24-47.
 RC TISSUE=Brain;
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 Ray N., Ratery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212 (1985).
 RN [5]
 RP MUTAGENESIS OF LEU-270.
 RX MEDLINE=92049732; PubMed=1719423;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RT "Mutations in the channel domain alter desensitization of a neuronal
 RT nicotinic receptor.";
 RL Nature 353:846-849 (1991).
 RN [6]
 RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RX MEDLINE=93024917; PubMed=1383929;
 RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
 Changeux J.-P., Bertrand D.;
 RT "Mutations in the channel domain of a neuronal nicotinic receptor
 RT convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505 (1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X52295; CAA36543.1; -;
 DR EMBL; X68246; CAA48317.1; -;
 DR EMBL; X68586; CAA48576.1; -;
 DR PIR; JN0113; JN0113.
 DR PIR; B25738; B25738.
 DR PIR; JH0172; JH0172.
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur. Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 KW Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23
 FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT EXTRACELLULAR.
 FT DOMAIN 24 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469
 FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT MUTAGEN 270 270
 FT CONFLICT 26 27
 FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
 SQ
 Query Match 18.3%; Score 92; DB 1; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-82;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 275 FMLLVAVIMPATSDVPLIAQYFASVTMIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVI 334
 DB 275 FMLLVAVIMPATSDVPLIAQYFASVTMIIVGLSVVTVIVLQYHHDDPGGKMPKWTIRVI 334
 OY 335 LLNWCWFLRMKRPGEKDVPRACQKQRCSL 366
 DB 335 LLNWCWFLRMKRPGEKDVPRACQKQRCSL 366
 RESULT 3
 ACH7_BOVIN
 ID ACH7_BOVIN STANDARD; PRT; 499 AA.
 AC P54131;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=95346009; PubMed=7620615;
 RA Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,
 Gutierrez L., Criado M.;

"Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine RT chromaffin cells: molecular cloning, functional expression and RT alternative splicing of the alpha 7 subunit.";
 Eur. J. Neurosci. 7:647-655(1995).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-B CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY CC SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO CC UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT CC FORMS OF THE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL: X93604; CAA63802.1; --
 CC InterPro: IPR000188; GABAA receptor.
 CC InterPro: IPR001175; Neur_chan_LBD.
 CC Pfam: PF02931; Neur_chan_LBD; 1.
 CC Pfam: PF02932; Neur_chan_memb; 1.
 CC PRINTS: PR00252; NRIONCHANNEL.
 CC TIGRFS: TIGR00860; LIC; 1.
 CC PROSITE: PS00236; NEUROTR ION CHANNEL; 1.
 CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family; Alternative splicing.
 CC SIGNAL 1 19 BY SIMILARITY.
 CC CHAIN 20 499 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 CC ALPHA-7 CHAIN.
 CC DOMAIN 20 227 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 228 252 POTENTIAL.
 CC TRANSMEM 259 277 POTENTIAL.
 CC TRANSMEM 293 314 POTENTIAL.
 CC DOMAIN 315 466 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 467 487 POTENTIAL.
 CC DISULFID 147 161 BY SIMILARITY.
 CC DISULFID 209 210 ASSOCIATED WITH RECEPTOR ACTIVATION
 CC (BY SIMILARITY).
 CC CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VARSPIC 262 290 MISSING (IN SHORT ISOFORM).
 CC SEQUENCE 499 AA; 56002 MW; AEE5D0B382D042D5 CRC64;
 CC -----
 CC Query Match 14.1%; Score 71; DB 1; Length 499;
 CC Best Local Similarity 100.0%; Pred. No. 6.6e-62;
 CC Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC 92 SEYPGVKTFRFPDQGIWKPDILLYNSADERFDATFHTNVLVNSGHCQYLPPIGFKSSCY 151
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 89 SEYPGVKTFRFPDQGIWKPDILLYNSADERFDATFHTNVLVNSGHCQYLPPIGFKSSCY 148
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 152 IDVRWPFDFVQ 162
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 149 IDVRWPFDFVQ 159
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC -----
 CC RESULT 4
 CC ACH7_MOUSE STANDARD; PRT; 502 AA.
 CC AC P49582;
 CC DT 01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CRNA7 OR ACRA7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 CC (1)
 CC SEQUENCE FROM N.A.
 CC STRAIN=BALB/c; TISSUE=Brain;
 CC MEDLINE=9534936; PubMed=7601470;
 CC Orr-Urtreger A., Seidini M.F., Baldini A., Beaudet A.L.;
 CC "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
 CC acetylcholine receptor.";
 CC Genomics 26:399-402(1995).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA CC MEMBRANE.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-B CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL: L37663; AAC42053.1; --
 CC MGD; MGI:997779; Chrna7.
 CC InterPro: IPR000188; GABAA receptor.
 CC InterPro: IPR001175; Neur_Channel.
 CC Pfam: PF02931; Neur_chan_LBD; 1.
 CC Pfam: PF02932; Neur_chan_memb; 1.
 CC PRINTS: PR00252; NRIONCHANNEL.
 CC TIGRFS: TIGR00860; LIC; 1.
 CC PROSITE: PS00236; NEUROTR ION CHANNEL; 1.
 CC Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family.
 CC SIGNAL 1 22 BY SIMILARITY.
 CC CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 CC ALPHA-7 CHAIN.
 CC DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 231 255 POTENTIAL.
 CC TRANSMEM 262 280 POTENTIAL.
 CC TRANSMEM 296 317 POTENTIAL.
 CC DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 470 490 POTENTIAL.
 CC DISULFID 150 164 BY SIMILARITY.
 CC DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 CC (BY SIMILARITY).
 CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;
 CC -----
 CC Query Match 12.4%; Score 62; DB 1; Length 502;
 CC Best Local Similarity 100.0%; Pred. No. 5e-53;
 CC Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC 29 LYKELVKYNPLRPVANDSQPLTVYFSLSLQIMDVDEKQVLTNNIWLQMSWDHYLQ 88
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 29 LYKELVKYNPLRPVANDSQPLTVYFSLSLQIMDVDEKQVLTNNIWLQMSWDHYLQ 88
 CC |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 89 WN 90
 CC |||||
 CC 89 WN 90

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RESULT 5
ACH7_RAT  ACH7_RAT  STANDARD;  PRT;  502 AA.
ID  Q05941;
AC  Q05941;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN  CHRNA7 OR ACHRA7.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_taxid=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RX  MEDLINE=93147911; PubMed=7678857;
RA  Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
RT  "Molecular cloning, functional properties, and distribution of rat
RT  brain alpha 7: a nicotinic cation channel highly permeable to
RT  calcium.";
RL  J. Neurosci. 13:596-604(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sprague-Dawley; TISSUE=Brain;
RA  Hartley M.;
RL  Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC  EXTENSIVE CHANGING IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC  LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC  MEMBRANE.
CC  -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC  BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC  SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; S53987; AAB25224.2; --
DR  EMBL; L31619; AAC33136.1; --
DR  InterPro; IPR000188; GABAA_receptor.
DR  InterPro; IPR001175; Neur Channel.
DR  Pfam; PF02931; Neur_chan_1BD; 1.
DR  Pfam; PF02932; Neur_chan_memb; 1.
DR  PRINTS; PR00252; NRIONCHANNEL.
DR  TIGRFAMS; TIGR00860; LIC; 1.
DR  PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW  Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal;
KW  Transmembrane; Multigene family.
FT  SIGNAL 1 22 BY SIMILARITY.
FT  CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT  ALPHA-7 CHAIN.
FT  DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 21 255 POTENTIAL.
FT  TRANSMEM 262 280 POTENTIAL.
FT  TRANSMEM 296 317 POTENTIAL.
FT  DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 470 490 POTENTIAL.
FT  DISULFID 150 164 BY SIMILARITY.

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FT  DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
FT  CARBOHYD 46 (BY SIMILARITY).
FT  CARBOHYD 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CONFLICT 447 N -> F (IN REF. 2).
FT  CONFLICT 469 P -> R (IN REF. 2).
SQ  SEQUENCE 502 AA; 56410 MW; 00996E74EC7B9A56 CRC64;

Query Match 12.4%; Score 62; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 5e-53;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LYKELVKYNYPLERPVANDSQPLTYVYFSLSLQIMDVDEKXQVLTNTIWLQMSWTDHYLQ 88
Db 29 LYKELVKYNYPLERPVANDSQPLTYVYFSLSLQIMDVDEKXQVLTNTIWLQMSWTDHYLQ 88
QY 89 WN 90
Db 89 WN 90

RESULT 6
SHT3_HUMAN
ID  SHT3_HUMAN STANDARD; PRT; 478 AA.
AC  P46098;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion
DE  channel receptor) (5-HT3R).
GN  HTR3A OR HTR3 OR 5HT3R.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_taxid=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Hippocampus;
RX  MEDLINE=96018832; PubMed=7565620;
RA  Miyake A., Mochizuki S., Takemoto Y., Akuzawa S.;
RT  "Molecular cloning of human 5-hydroxytryptamine3 receptor:
RT  heterogeneity in distribution and function among species.";
RL  Mol. Pharmacol. 48:407-416(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Amygdala;
RX  MEDLINE=99127223; PubMed=9928262;
RA  Bruss M., Gothert M., Hayer M., Bonisch H.;
RT  "Molecular cloning of alternatively spliced human 5HT3 receptor
RT  cDNAs.";
RL  Ann. N.Y. Acad. Sci. 861:234-235(1998).
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Publ H.L. III, Ikeda S.R., Aronstam R.S.;
RL  Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN  [4]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lung;
RA  Strausberg R.;
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
CC  5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
CC  AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS
CC  A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST,
CC  DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT
CC  OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC  -----
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EMBL; D49394; BAA08387.1; -;
 EMBL; AF003079; CAA05852.1; -;
 EMBL; AF498984; AAM21131.1; -;
 EMBL; BC002354; AAO02354.1; -;
 Genew; HGNC:5297; HTR3A.
 MIM; 182133; -;
 InterPro; IPR000188; GABAA_receptor.
 InterPro; IPR001175; Neur_Channel.
 Pfam; PF02931; Neur_chan_LBD; 1.
 Pfam; PF02932; Neur_chan_memb; 1.
 PRINTS; PR00252; NRIONCHANNEL.
 TIGRPFMS; TIGR00860; LIC; 1.
 PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 Transmembrane; Receptor; Glycoprotein; Signal;
 Phosphorylation.
 SIGNAL 1 23 POTENTIAL
 CHAIN 24 478 5-HYDROXYTRYPTAMINE 3 RECEPTOR.
 DOMAIN 24 241 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 242 268 1 (POTENTIAL).
 DOMAIN 269 273 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 274 292 2 (POTENTIAL).
 DOMAIN 293 302 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 303 321 3 (POTENTIAL).
 DOMAIN 322 455 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 456 475 4 (POTENTIAL).
 DOMAIN 476 478 EXTRACELLULAR (POTENTIAL).
 DISULFID 157 171 BY SIMILARITY.
 CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 478 AA; 55280 MW; 24CA9A232286FBC9 CRC64;

Query Match 2.0%; Score 10; DB 1; Length 478;

Best Local Similarity 100.0%; Pred. No. 0.088;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 65 VDEKNOVLTT 74

|||||

73 VDEKNOVLTT 82

RESULT 7

ACH9 HUMAN STANDARD; PRT; 479 AA.
 AC Q9UGM1; Q9NVV2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-9 chain precursor.
 GN CHR9A9 OR NACHRA9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Chantier E., Partisetti M., Besnard F., Sgard F.;
 RT "Cloning and characterization of the human alpha 9 nicotinic
 RT acetylcholine receptor."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 7-476 FROM N.A.
 RA Nguyen Thuong V., Grando S.A.;
 RT "Cloning and characterization of human alpha 9 nicotinic acetylcholine
 RT receptor subunit from normal oral epithelial cell."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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EMBL; AJ243342; CAB65091.1; -;
 EMBL; AF227732; AAF61920.1; -;
 Genew; HGNC:14079; CHR9A9.
 MIM; 605116; -;
 InterPro; IPR000188; GABAA_receptor.
 InterPro; IPR001175; Neur_Channel.
 Pfam; PF02931; Neur_chan_LBD; 1.
 Pfam; PF02932; Neur_chan_memb; 1.
 PRINTS; PR00252; NRIONCHANNEL.
 TIGRPFMS; TIGR00860; LIC; 1.
 PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 Transmembrane; Multigene family.
 SIGNAL 1 25 POTENTIAL.
 CHAIN 26 479 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 ALPHA-9 CHAIN.
 DOMAIN 26 237 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 238 262 POTENTIAL.
 TRANSMEM 269 287 POTENTIAL.
 TRANSMEM 302 323 POTENTIAL.
 DOMAIN 324 457 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 458 476 POTENTIAL.
 DISULFID 155 169 BY SIMILARITY.
 DISULFID 219 220 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CONFLICT 442 442 S -> N (IN REF. 2).
 SEQUENCE 479 AA; 54780 MW; 336B46B559C6FF13 CRC64;

Query Match 2.0%; Score 10; DB 1; Length 479;

Best Local Similarity 100.0%; Pred. No. 0.088;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 236 NLLIPCVLIS 245

|||||

243 NLLIPCVLIS 252

RESULT 8

ACH9 RAT STANDARD; PRT; 479 AA.
 ID ACH9 RAT
 AC P43144;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-9 chain precursor.
 GN CHR9A9 OR ACHRA9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=95042767; PubMed=7954834;
 RA Elgoyhen A.B., Johnson D.S., Boulter J., Vetter D.E., Heinemann S.F.;

RT "Alpha 9: an acetylcholine receptor with novel pharmacological
 RL properties expressed in rat cochlear hair cells.";
 CC Cell 79:705-715(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- FUNCTION: IS INVOLVED IN THE CHOLINERGIC EFFERENT INNERVATION OF
 CC COCHLEAR HAIR CELLS AND THUS MAY MODULATE THE ENCODING OF AUDITORY
 CC STIMULI. THIS RECEPTOR POSSESSES BOTH NICOTINIC AND MUSCARINIC
 CC PROPERTIES.
 CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: DETECTED IN THE NASAL EPITHELIUM, IN THE OUTER
 CC HAIR CELLS OF THE COCHLEA, IN THE PARS TUBERALEM OF THE
 CC HYPOTHYSLIS, AND IN THE DEVELOPING MUSCLE OF THE TONGUE.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL; U12336; AAA56720.1; --
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Post-synaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 479 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-9 CHAIN.
 FT DOMAIN 26 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 262 POTENTIAL.
 FT TRANSMEM 269 287 POTENTIAL.
 FT TRANSMEM 302 323 POTENTIAL.
 FT DOMAIN 324 457 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 458 476 POTENTIAL.
 FT DISULFID 155 169 BY SIMILARITY.
 FT DISULFID 219 220 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 479 AA; 54495 MW; CBAGF45B9DF69287 CRC64;
 Query Match 2.0%; Score 10; DB 1; Length 479;
 Best Local Similarity 100.0%; Pred. No. 0.088;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 236 NLLIPCVLIS 245
 |||||
 Db 243 NLLIPCVLIS 252
 RESULT 9
 SHT3_RAT
 ID SHT3_RAT STANDARD; PRT; 483 AA.
 AC P35563;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion
 GN channel receptor) (5-HT3R).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Miyake A., Mochizuki S., Akuzawa S., Kon G.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE OF 22-483 FROM N.A.
 RX MEDLINE=94154206; PubMed=7509203;
 RA Isenberg K.E., Ukun I.A., Holstad S.G., Jafri S., Uchida U.,
 RA Zorumski C.F., Yang J.;
 RT "Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor
 RT subunit.";
 RL NeuroReport 5:121-124(1993).
 CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
 CC 5-HYDROXYTRYPTAMINE (SEROTONIN). A BIOGENIC HORMONE THAT FUNCTION
 CC AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS
 CC A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST, BUT
 CC DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT
 CC OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 CC EMBL; D49395; BAA08388.1; --
 DR EMBL; U01227; AAA52182.1; --
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Ionic channel; Transmembrane; Receptor; Glycoprotein; Signal;
 KW Phosphorylation.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 483 5-HYDROXYTRYPTAMINE 3 RECEPTOR.
 FT DOMAIN 24 246 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 247 273 1 (POTENTIAL).
 FT TRANSMEM 274 278 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 279 297 2 (POTENTIAL).
 FT DOMAIN 298 307 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 308 326 3 (POTENTIAL).
 FT DOMAIN 327 460 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 461 480 4 (POTENTIAL).
 FT DOMAIN 481 483 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 162 176 BY SIMILARITY.
 FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 22 22 E -> K (IN REF. 2).
 FT CONFLICT 306 306 G -> R (IN REF. 2).
 SQ SEQUENCE 483 AA; 55428 MW; ED85257BBCCF28A4 CRC64;
 Query Match 2.0%; Score 10; DB 1; Length 483;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 65 VDEKNQVLTT 74
 |||||
 Db 78 VDEKNQVLTT 87
 RESULT 10
 SHT3_MOUSE

ID 5HT3 MOUSE STANDARD; PRT; 487 AA.
 AC P23979; Q61225; Q61226;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion
 channel receptor) (5-HT3R).
 GN HTR3A OR HTR3 OR 5HT3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92022603; PubMed=1718042;
 RA Maricq A.V., Peterson A.S., Brake A.J., Myers R.M., Julius D.;
 RT "Primary structure and functional expression of the 5HT3 receptor, a
 serotonin-gated ion channel.";
 RL Science 254:432-437(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Brain;
 RX MEDLINE=94156052; PubMed=8112471;
 RA Uetz P., Abdelatty F., Villarroel A., Gundrun R., Weiss B., Koenen M.;
 RT "Organisation of the murine 5-HT3 receptor gene and assignment to
 human chromosome 11.";
 RL FEBS Lett. 339:302-306(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=93259238; PubMed=7683998;
 RA Hope A.G., Downie D.L., Sutherland L., Lambert J.J., Peters J.A.,
 Burchell B.;
 RT "Cloning and functional expression of an apparent splice variant of
 the murine 5-HT3 receptor A subunit.";
 RL Eur. J. Pharmacol. 245:187-192(1993).
 RN [4]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=129/Sv;
 RX MEDLINE=95157178; PubMed=7854052;
 RA Werner P., Kawashima E., Reid J., Hussy N., Lundstrom K., Buell G.,
 Humbert Y., Jones K.A.;
 RT "Organization of the mouse 5-HT3 receptor gene and functional
 expression of two splice variants.";
 RL Brain Res. Mol. Brain Res. 26:233-241(1994).
 CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR
 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTION
 AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THIS RECEPTOR IS
 A LIGAND-GATED ION CHANNEL, WHICH WHEN ACTIVATED CAUSES FAST,
 DEPOLARIZING RESPONSES IN NEURONS. IT IS A CATION-SPECIFIC, BUT
 OTHERWISE RELATIVELY NONSELECTIVE, ION CHANNEL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5-HT3R-A (SHOWN HERE) AND 5-
 HT3R-AS; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, AND HEART.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M74425; AAA37124.1; -
 DR EMBL; Z22772; CAA80453.1; -
 DR EMBL; Z22773; CAA80453.1; JOINED.
 DR EMBL; X72395; CAA51089.1; -
 DR EMBL; X79283; CAA55870.1; -
 DR EMBL; X79283; CAA55871.1; -
 DR PIR; A40832; A40832.
 DR MGD; MGI:96282; Htr3a.

DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NR1ONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
 DR Ionic channel; Transmembrane; Receptor; Glycoprotein; Signal;
 KW Phosphorylation; Alternative splicing.
 FT SIGNAL 1 23
 FT CHAIN 24 487
 FT DOMAIN 24 245
 FT TRANSMEM 246 272
 FT DOMAIN 273 277
 FT TRANSMEM 278 296
 FT DOMAIN 297 305
 FT TRANSMEM 306 324
 FT DOMAIN 325 464
 FT TRANSMEM 465 484
 FT DOMAIN 485 487
 FT DISULFID 161 175
 FT CARBOHYD 108 108
 FT CARBOHYD 174 174
 FT CARBOHYD 190 190
 FT VARSPIC 383 388
 FT CONFLICT 31 31
 FT CONFLICT 74 74
 FT CONFLICT 302 302
 FT CONFLICT 384 384
 FT CONFLICT 393 393
 FT CONFLICT H -> T (IN REF. 4).
 SQ SEQUENCE 487 AA; 56056 MW; D0148867C8536D66 CRC64;
 Query Match 2.0%; Score 10; DB 1; Length 487;
 Best Local Similarity 100.0%; Pred. No. 0.09;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 65 VDEKNQVLTT 74
 DB 77 VDEKNQVLTT 86
 RESULT 11
 ACHX ONCVO STANDARD; PRT; 436 AA.
 AC P54247;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, non-alpha chain (Fragment).
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94299155; PubMed=8026747;
 RA Ajun P.M., Egwang T.G.;
 RT "Cloning of a cDNA encoding a putative nicotinic acetylcholine
 receptor subunit of the human filarial parasite Onchocerca
 volvulus.";
 RL Gene 144:127-129(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
 RT "Nicotinic acetylcholine receptors in the nematode *Caenorhabditis*
 RL *elegans*."; J. Mol. Biol. 258:261-269(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Nelson J., Wohlmann P.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 DR EMBL; X83887; CAA58764.1; -;
 DR EMBL; AF022973; AAC25796.1; -;
 DR HSP; P58154; I19B.
 DR WormPep; F25G6.3; CE09639.
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT
 FT DOMAIN 20 230
 FT TRANSMEM 231 252
 FT TRANSMEM 261 279
 FT TRANSMEM 295 314
 FT DOMAIN 315 472
 FT TRANSMEM 473 493
 FT DISULFID 147 161
 FT DISULFID 211 212
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 93 93
 FT SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;
 SQ
 Query Match 1.8%; Score 9; DB 1; Length 498;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 226 MRRRTLYYG 234
 DB 225 MRRRTLYYG 233
 RESULT 14
 ACH5 CAEEL
 ID ACH5 CAEEL STANDARD; PRT; 511 AA.
 AC Q23022; Q17408; P91265; O02559;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor, alpha-type subunit unc-38 precursor.
 GN UNC-38 OR F21F3.5.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 OX NCBI_TaxID=6239;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=97368239; PubMed=9221782;
 RA Fleming J.T., Squire M.D., Barnes T.M., Tornoe C., Matsuda K.,
 RA Annn J., Fire A., Sulston J.E., Barnard E.A., Sattelle D.B.,
 RA Lewis J.A.;
 RT "Caenorhabditis elegans levamisole resistance genes lev-1, unc-29,
 RT and unc-38 encode functional nicotinic acetylcholine receptor
 RT subunits."; J. Neurosci. 17:5843-5857(1997).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Geisel C., Kramer J., Elliott G.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP REVISIONS.
 RA Waterston R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ACETYLCHOLINE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 CC
 DR EMBL; X98600; CAA67197.1; -;
 DR EMBL; X98599; CAA67196.1; -;
 DR EMBL; U88175; AAB42282.2; -;
 DR WormPep; F21F3.5; CE09535.
 DR InterPro; IPR000188; GABAA receptor.
 DR InterPro; IPR001175; Neur Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 511
 FT
 FT DOMAIN 17 261
 FT TRANSMEM 262 282
 FT TRANSMEM 291 311
 FT TRANSMEM 324 344
 FT DOMAIN 345 464
 FT TRANSMEM 465 485
 FT DISULFID 151 165
 FT DISULFID 238 239
 FT CARBOHYD 124 124
 FT CARBOHYD 202 202
 FT SEQUENCE 511 AA; 59454 MW; 19F690731B23E1A6 CRC64;
 SQ
 Query Match 1.8%; Score 9; DB 1; Length 511;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 152 IDVRWFFPD 160
 DB 153 IDVRWFFPD 161
 RESULT 15
 ACH1 SCHGR
 ID ACH1 SCHGR STANDARD; PRT; 557 AA.
 AC P23414;
 DT 01-NOV-1991 (Rel. 20, Created)

```

DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-L1 chain precursor.
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092263; PubMed=1702381;
RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RT insect nicotinic acetylcholine receptor.";
RL EMBO J. 9:4391-4398(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
DR EMBL; X55439; CAA39081.1; -.
DR PIR; S12359; S12359.
DR InterPro; IPR000188; GABAA receptor.
DR InterPro; IPR001175; Neur_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT FT CHAIN EXTRACELLULAR.
FT DOMAIN 24 244
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500 CYTOPLASMIC.
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT FT CARBOHYD 47 47
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 382 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 406 422 ALA/SER-RICH.
FT SEQUENCE 557 AA; 63026 MW; 168389C87DFDF3E CRC64;

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Query Match 1.8%; Score 9; DB 1; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 254 LPADSGEKI 262
 |||||
 Db 266 LPADSGEKI 274

Search completed: June 20, 2003, 19:12:10
 Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:09:27 ; Search time 43 Seconds
(without alignments)
1122.313 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 502
Sequence: 1 MRCSPGGVWLAAASLLHVS.....TIGILSGAPNEAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2355

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	289	57.6	502	1 ACHUA7	nicotinic acetylch
2	267	53.2	502	2 GQ2259	alpha 7 neuronal n
3	92	18.3	502	2 JN0113	nicotinic acetylch
4	62	12.4	502	2 T01378	nicotinic receptor
5	62	12.4	502	2 A51775	nicotinic acetylch
6	27	5.4	511	2 JH0173	alpha-bungarotoxin
7	12	2.4	565	2 T23843	hypothetical prote
8	11	2.2	456	2 T24504	hypothetical prote
9	10	2.0	462	2 I58179	5HT3 receptor subu
10	10	2.0	479	2 A55382	nicotinic acetylch
11	10	2.0	489	2 S41757	5-hydroxytryptamin
12	10	2.0	542	2 T19862	hypothetical prote
13	9	1.8	336	2 T16652	hypothetical prote
14	9	1.8	466	2 PC4296	nicotinic acetylch
15	9	1.8	498	2 S68598	nicotinic acetylch
16	9	1.8	511	2 T43634	nicotinic acetylch
17	9	1.8	534	2 T25720	hypothetical prote
18	9	1.8	557	2 S12359	nicotinic acetylch
19	9	1.8	576	1 ACPFA2	nicotinic acetylch
20	8	1.6	113	2 S56647	trypsin inhibitor
21	8	1.6	113	2 S56648	trypsin inhibitor
22	8	1.6	141	2 A40463	integrin alpha-6 c
23	8	1.6	149	2 B40463	integrin alpha-6 c
24	8	1.6	245	2 C64616	hypothetical prote
25	8	1.6	356	2 D86382	hypothetical prote
26	8	1.6	416	1 ACCH3N	nicotinic acetylch
27	8	1.6	452	2 D83609	probable glutamine
28	8	1.6	461	2 T25671	hypothetical prote
29	8	1.6	513	1 ACCHD1	nicotinic acetylch

30 8 1.6 517 2 A60916 nicotinic acetylch
31 8 1.6 521 2 C28529 nicotinic acetylch
32 8 1.6 559 2 E89134 protein F25G6.4 [i
33 8 1.6 560 2 T19622 hypothetical prote
34 8 1.6 567 1 ACPFA1 nicotinic acetylch
35 8 1.6 1072 2 A38457 integrin alpha-6 c
36 7 1.4 68 2 G69093 histone HMTA2 - Me
37 7 1.4 69 2 A35959 archaean histone H
38 7 1.4 101 2 E75487 v-type ATP synthas
39 7 1.4 116 2 T05366 auxin-induced prot
40 7 1.4 127 2 B97810 cytochrome P450 CY
41 7 1.4 128 2 S70623 cytochrome P450 CY
42 7 1.4 130 2 G25733 T-cell receptor al
43 7 1.4 130 2 E87384 cytochrome c famil
44 7 1.4 143 2 E86824 hypothetical prote
45 7 1.4 144 2 S01898 psIB protein - Esc

ALIGNMENTS

RESULT 1

ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)

C>Date: 12-Aug-1996 #sequence revision 31-Jan-1997 #text_change 22-Jun-1999

C:Accession: I37185; A54194; S60309

R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.

Mol. Pharmacol. 45, 546-554, 1994

A>Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the

omers expressed in Xenopus oocytes.

A:Reference number: I37185; MUID:94195283; PMID:8145738

A:Accession: I37185

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-502 <PEN>

A:Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607

A:Experimental source: Brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A>Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotinic

A:Reference number: A54194; MUID:94245214; PMID:8188270

A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737

A:Experimental source: retina

C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized

C:Genetics:

A:Gene: GDB:CHRNA7

A:Cross-references: GDB:138751; OMIM:118511

A:Map position: 15q14-15q14

A>Note: defects in this gene have been associated with mental retardation and schizophrenia

C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains a

C:Superfamily: acetylcholine receptor

C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter receptor

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred

F:231-254/Domain: transmembrane #status predicted <TR1>

F:262-280/Domain: transmembrane #status predicted <TR2>

F:296-317/Domain: transmembrane #status predicted <TR3>

F:470-488/Domain: transmembrane #status predicted <TR4>

F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Bisulfide bonds: #status predicted

F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted

F:415/Binding site: phosphate (Thr) (covalent) #status predicted

F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

Best Local Similarity 57.6%; Score 289; DB 1; Length 502;

Matches 489; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 LAASLLHVSQGBFQKLYKELVKNYNPLRPVANDSQPLTVTVFSLLQIMDVDEKQV 71
 Db 12 LAASLLHVSQGBFQKLYKELVKNYNPLRPVANDSQPLTVTVFSLLQIMDVDEKQV 71
 QY 72 LTTNIWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNLSADERFDFATFHTNVL 131
 Db 72 LTTNIWLQSWTDHYLQWNVSEYPGVKTVPDGOIWKPDILLYNLSADERFDFATFHTNVL 131
 QY 132 VNSSGHCOYLPPGIFKSSCYIDVRWPFVQHCCKLFGWSYSGWSLDLQWQAEADISGYI 191
 Db 132 VNSSGHCOYLPPGIFKSSCYIDVRWPFVQHCCKLFGWSYSGWSLDLQWQAEADISGYI 191
 QY 192 PNGEWDLVGIPIGRKSERFECCKEPYPDVFTVTMRRTLYYGLNLLIPCVLISALALLV 251
 Db 192 PNGEWDLVGIPIGRKSERFECCKEPYPDVFTVTMRRTLYYGLNLLIPCVLISALALLV 251
 QY 252 FILPADSGEKISGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVT 311
 Db 252 FILPADSGEKISGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVT 311
 QY 312 VIVLQVHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEM 371
 Db 312 VIVLQVHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEM 371
 QY 372 SAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPTHDEHLLHGGQPPGDP 431
 Db 372 SAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPTHDEHLLHGGQPPGDP 431
 QY 432 DLAKILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAP 491
 Db 432 DLAKILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAP 491
 QY 492 NFVEAVSKDFA 502
 Db 492 NFVEAVSKDFA 502

RESULT 2

G02259
 alpha 7 neuronal nicotinic acetylcholine receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
 C:Accession: G02259
 R:Leonard, S.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: H00936
 A:Accession: G02259
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <LEO>
 A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
 C:Superfamily: acetylcholine receptor

Query Match 53.2%; Score 267; DB 2; Length 502;
 Best Local Similarity 99.7%; Pred. No. 3.7e-259;
 Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 SGHCQYLPPGIFKSSCYIDVRWPFVQHCCKLFGWSYSGWSLDLQWQAEADISGYIPNG 194
 Db 135 SGHCQYLPPGIFKSSCYIDVRWPFVQHCCKLFGWSYSGWSLDLQWQAEADISGYIPNG 194
 QY 195 EMDLVGIPIGRKSERFECCKEPYPDVFTVTMRRTLYYGLNLLIPCVLISALALLV 254
 Db 195 EMDLVGIPIGRKSERFECCKEPYPDVFTVTMRRTLYYGLNLLIPCVLISALALLV 254
 QY 255 PADSGEKISGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVTIV 314
 Db 255 PADSGEKISGITVLLSLTFVMLLVAEIMPATSDSVPLIAQYFASFTMIIVGLSVVVTIV 314
 QY 315 LOYHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEMSAV 374
 Db 315 LOYHHDDPGGKMPKTRVILLNWCAMFLMRKRPGEKVRPACQHKORRCSLASVEMSAV 374

QY 375 APPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPTHDEHLLHGGQPPGDPDLA 434
 Db 375 APPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGMACSPTHDEHLLHGGQPPGDPDLA 434
 QY 435 KILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAPNFV 494
 Db 435 KILEEVYIANRFRQDESEAVCEWKFACVDRCLCLMAPSVFTIICITIGILMSAPNFV 494
 QY 495 EAVSKDFA 502
 Db 495 EAVSKDFA 502

RESULT 3

JN0113
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
 N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
 C:Species: Gallus gallus (chicken)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
 C:Accession: JN0113; JH0172; S28018; B25738; S26566
 R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990
 A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmental
 A:Reference number: JN0113; MUID:91097796; PMID:1702646
 A:Accession: JN0113
 A:Molecule type: DNA
 A:Residues: 1-502 <COU>
 A:Cross-references: GB:X68596; NID:g287756; PIDN:CAA48576.1; PID:g287757
 A:Experimental source: white leghorn; brain
 R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAb reveal subtypes of thi
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0172
 A:Molecule type: mRNA
 A:Residues: 1-502 <SCH>
 A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
 A:Experimental source: brain
 R:Matter-Sadzinski, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M.
 EMBO J. 11, 4529-4538, 1992
 A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter d
 A:Reference number: S28018; MUID:93049204; PMID:1425587
 A:Accession: S28018
 A:Molecule type: DNA
 A:Residues: 1-18 <MAS>
 A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
 A:Experimental source: white leghorn; erythrocyte
 R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; R
 Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
 A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologou
 A:Reference number: A94055; MUID:85270494; PMID:3860855
 A:Accession: B25738
 A:Molecule type: protein
 A:Residues: 24-25,'ET',28-41,'X',43-45,'X',47 <CON>
 C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
 C:Genetics:
 A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
 C:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pred
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:476,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.3%; Score 92; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.1e-83;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 FMLLVAEIMPATSDVPLIAQYFASFTMLIVGLSVVVTVIVLYOYHHDDPGGKMPKWTTRVI 334
 |||||
 Db 275 FMLLVAEIMPATSDVPLIAQYFASFTMLIVGLSVVVTVIVLYOYHHDDPGGKMPKWTTRVI 334
 |||||
 Qy 335 LLNWCWFLRMKRPGEKVRPACQKORRCSL 366
 |||||
 Db 335 LLNWCWFLRMKRPGEKVRPACQKORRCSL 366
 |||||

RESULT 4

T01378
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T01378
 R:Seguela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
 J. Neurosci. 13, 596-604, 1993
 A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7
 A:Reference number: Z14310; MUID:93147931; PMID:7678857
 A:Accession: T01378
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-502 <SEG>
 A:Cross-references: EMBL:S53987; NID:G264770; PIDN:AAB25224.2; PID:G5705903
 A:Experimental source: brain
 C:Superfamily: acetylcholine receptor

Query Match 12.4%; Score 62; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-53;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Db 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||

Qy 89 WN 90
 ||
 Db 89 WN 90
 ||

RESULT 5

A57175
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:I37663; NID:G790853; PIDN:AAC42053.1; PID:G790854
 A:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
 F:231-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 12.4%; Score 62; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.3e-53;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Db 29 LYKELVKNYNPLERPANDSOPLTIVYFSLSLQIMDVDEKKNQVLTNNIWLQMSWTDHYLQ 88
 |||||
 Qy 89 WN 90
 ||
 Db 89 WN 90
 ||

RESULT 6

JH0173
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
 C:Accession: JH0173
 R:Schoeffer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal subtypes of thi
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0173
 A:Molecule type: mRNA
 A:Residues: 1-511 <SCH>
 A:Cross-references: GB:X52296; NID:G63081; PIDN:CAA36544.1; PID:G63082
 A:Experimental source: brain
 A:Note: this sequence is similar to acetylcholine receptor alpha chains
 C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudoden
 C:Superfamily: acetylcholine receptor
 C:Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <A
 F:239-282/Domain: transmembrane #status predicted <TM1>
 F:270-288/Domain: transmembrane #status predicted <TM2>
 F:304-323/Domain: transmembrane #status predicted <TM3>
 F:479-496/Domain: transmembrane #status predicted <TM4>
 F:54/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 5.4%; Score 27; DB 2; Length 511;
 Best Local Similarity 100.0%; Pred. No. 1.6e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LALLVFLLPADSGEKISIGITVLLSLT 273
 |||||
 Db 255 LALLVFLLPADSGEKISIGITVLLSLT 281
 |||||

RESULT 7

T23843
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T23843
 R:Coles, L.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19807
 A:Accession: T23843
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-565 <WML>
 A:Cross-references: EMBL:Z68118; PIDN:CAA92184.1; GSPDB:GN00028; CESP:R01E6.4
 A:Experimental source: clone R01E6
 C:Genetics:
 A:Map position: X
 A:Map position: 43/3; 84/3; 121/2; 155/3; 190/1; 253/2; 300/3; 364/2; 398/3; 444/3; 500/3
 A:Introns: 43/3; 84/3; 121/2; 155/3; 190/1; 253/2; 300/3; 364/2; 398/3; 444/3; 500/3
 C:Superfamily: acetylcholine receptor

Query Match 2.4%; Score 12; DB 2; Length 565;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 DVDEKKNQVLTNN 75
 |||||
 Db 68 DVDEKKNQVLTNN 79
 |||||

RESULT 8

T24504
Hypothetical protein T05C12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24504
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19901
A:Accession: T24504
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-456 <WIL>
A:Cross-references: EMBL:Z66500; PIDN:CRA91304.1; GSPDB:GN00020; CESP:T05C12.2
A:Experimental source: clone T05C12
C:Genetics:
A:Gene: CESP:T05C12.2
A:Map position: 2
A:Introns: 30/3; 75/3; 99/1; 117/2; 151/3; 189/1; 249/1; 314/3; 379/1; 416/3
C:Superfamily: acetylcholine receptor

Query Match 2.2%; Score 11; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 QIMDVDEKNQV 71

|||||

Db 56 QIMDVDEKNQV 66

RESULT 9

I58179
5HT3 receptor subunit - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58179
R:Isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Yan
Neuroreport 5, 121-124, 1993
A:Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit.
A:Reference number: I58179; MUID:94154206; PMID:7509203
A:Accession: I58179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-462 <RES>
A:Cross-references: EMBL:U01227; NID:9402245; PIDN:AAA52182.1; PID:9402246
C:Superfamily: acetylcholine receptor

Query Match 2.0%; Score 10; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74

|||||

Db 57 VDEKNQVLTT 66

RESULT 10

A55382
nicotinic acetylcholine receptor alpha-9 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 20-Aug-1999
C:Accession: A55382
R:Elgoyhen, A.B.; Johnson, D.S.; Boulter, J.; Vetter, D.E.; Heinemann, S.
Cell 79, 705-715, 1994
A:Title: alpha9: an acetylcholine receptor with novel pharmacological properties expressed in *Xenopus* oocytes
A:Reference number: A55382; MUID:95042767; PMID:7954834
A:Accession: A55382
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-479 <ELG>
A:Cross-references: GB:U12336; NID:G595480; PIDN:AAA56720.1; PID:G595481

C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 2.0%; Score 10; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 NLLIPCVLIS 245

|||||

Db 243 NLLIPCVLIS 252

RESULT 11

S41757
5-hydroxytryptamine-3 receptor - mouse
N:Alternate names: serotonin-gated ion channel 5HT3
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 05-Nov-1999
C:Accession: S41757; S43205; S48111; S45019; S40832; I48229; I48230
R:Uetz, P.; Abdelatty, F.; Villarroel, A.; Rappold, G.; Weiss, B.; Koenen, M.
FEBS Lett. 339, 302-306, 1994
A:Title: Organisation of the murine 5-HT(3) receptor gene and assignment to human chromosome 14
A:Reference number: S41757; MUID:94156052; PMID:8112471
A:Accession: S41757
A:Molecule type: DNA
A:Residues: 1-489 <UET1>
A:Cross-references: EMBL:Z22772
A:Note: the authors translated the codon TAC for residue 142 as His, GTG for residue 144
R:Uetz, P.
submitted to the EMBL Data Library, May 1993
A:Reference number: S43205
A:Accession: S43205
A:Molecule type: DNA
A:Residues: 1-30, 'E', 33-303, 305-311, 'I', 313-385, 'T', 387-489 <UET2>
A:Cross-references: EMBL:Z22772
R:Hope, A.G.; Downie, D.L.; Sutherland, L.; Lambert, J.J.; Peters, J.A.; Burchell, B.
Eur. J. Pharmacol. 245, 187-192, 1993
A:Title: Cloning and functional expression of an apparent splice variant of the murine 5-HT3 receptor
A:Reference number: S48111; MUID:93259238; PMID:7683998
A:Accession: S48111
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-74, 'V', 76-384, 391-489 <HOP>
A:Cross-references: EMBL:X72395; NID:G313863; PIDN:CAA51089.1; PID:G313864
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R:Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.
submitted to the EMBL Data Library, May 1994
A:Description: Organization of the mouse 5HT3 receptor gene and functional expression in *Xenopus* oocytes
A:Reference number: S45019
A:Accession: S45019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394, 'T', 396-489 <WER>
A:Cross-references: EMBL:X79283; NID:G488693; PIDN:CAA55871.1; PID:G488695
R:Maricq, A.V.; Peterson, A.S.; Brake, A.J.; Myers, R.M.; Julius, D.
Science 254, 432-437, 1991
A:Title: Primary structure and functional expression of the 5HT-3 receptor, a serotonin receptor
A:Reference number: A40832; MUID:92022603; PMID:1718042
A:Accession: A40832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-7, 'G', 8-30, 'E', 33-303, 305-489 <MAR>
A:Cross-references: GB:M74425
R:Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.
Brain Res. Mol. Brain Res. 26, 233-241, 1994
A:Title: Organization of the mouse 5-HT3 receptor gene and functional expression of two
A:Reference number: I48229; MUID:95157178; PMID:7854052
A:Accession: I48229

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-384,391-394,T',396-489 <RES>
 A:Cross-references: EMBL:X9283; NID:g488693; PIDN:CAA55871.1; PID:g488695
 A:Accession: I48230
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-394,T',396-489 <RE2>
 A:Cross-references: EMBL:X9283; NID:g488693; PIDN:CAA55870.1; PID:g488694
 C:Genetics:
 A:Introns: 23/1; 78/3; 93/3; 130/2; 187/1; 240/3; 311/1; 385/1
 C:Superfamily: acetylcholine receptor
 C:Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane
 F:247-273/Domain: transmembrane #status predicted <TM1>
 F:279-297/Domain: transmembrane #status predicted <TM2>
 F:308-326/Domain: transmembrane #status predicted <TM3>
 F:467-486/Domain: transmembrane #status predicted <TM4>

Query Match 2.0%; Score 10; DB 2; Length 489;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 VDEKNQVLTT 74
 |||||
 DB 78 VDEKNQVLTT 87
 |||||

RESULT 12
 T19862
 hypothetical protein C40C9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T19862
 R:Hembry, C.
 submitted to the EMBL Data Library, March 1996
 A:Reference number: Z19188
 A:Accession: T19862
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-542 <WIL>
 A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
 A:Experimental source: Clone C40C9
 C:Genetics:
 A:Gene: CESP:C40C9.2
 A:Map position: X
 A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49

Query Match 2.0%; Score 10; DB 2; Length 542;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 RRTLYYGLNL 237
 |||||
 DB 242 RRTLYYGLNL 251
 |||||

RESULT 13
 T16652
 hypothetical protein R02E12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 19-May-2000
 C:Accession: T16652
 R:Leinbach, D.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid R02E12.
 A:Reference number: Z18554
 A:Accession: T16652
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <LEI>
 A:Cross-references: EMBL:U53337; NID:g1255833; PID:g1255839; PIDN:AAA96188.1; GSPDB:GN00

C:Genetics:
 A:Gene: CESP:R02E12.1
 A:Map position: X
 A:Introns: 11/3; 26/3; 138/1; 183/2; 222/1; 251/1
 C:Superfamily: acetylcholine receptor

Query Match 1.8%; Score 9; DB 2; Length 336;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 PDILLYNSA 118
 |||||
 DB 58 PDILLYNSA 66
 |||||

RESULT 14
 PC4296
 nicotinic acetylcholine receptor alpha chain - nematode (Trichostrongylus colubriformis)
 N:Alternate names: tar-1 protein
 C:Species: Trichostrongylus colubriformis
 C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Aug-1998
 C:Accession: PC4296
 R:Wiley, L.J.; Weiss, A.S.; Sangster, N.C.; Li, Q.
 Gene 182, 97-100, 1996
 A:Title: Cloning and sequence analysis of the candidate nicotinic acetylcholine receptor
 A:Reference number: PC4296; MUID:9713696; PMID:8982073
 A:Accession: PC4296
 A:Molecule type: DNA
 A:Residues: 1-466 <WIL>
 A:Cross-references: GB:U56903
 C:Genetics:
 A:Gene: tar-1
 C:Superfamily: acetylcholine receptor
 F:214-239/Domain: transmembrane #status predicted <TM1>
 F:247-270/Domain: transmembrane #status predicted <TM2>
 F:276-299/Domain: transmembrane #status predicted <TM3>
 F:415-436/Domain: transmembrane #status predicted <TM4>

Query Match 1.8%; Score 9; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 IDVRWFPPD 160
 |||||
 DB 110 IDVRWFPPD 118
 |||||

RESULT 15
 S68588
 nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis
 C:Species: Caenorhabditis elegans
 C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
 C:Accession: S68588; S57496
 R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
 J. Mol. Biol. 258, 261-269, 1996
 A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
 A:Reference number: S68587; MUID:96196478; PMID:8627624
 A:Accession: S68588
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-498 <BAL>
 A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
 C:Superfamily: acetylcholine receptor
 C:Keywords: Glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT

Query Match 1.8%; Score 9; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MRRRTLYYG 234
 |||||

Db 225 MRRRTLYG 233

Search completed: June 20, 2003, 19:14:28
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:13:47 ; Search time 50 Seconds
(without alignments)
1086.396 Million cell updates/sec

Title: US-09-954-936-2
Perfect score: 502
Sequence: 1 MRCSPGGVWLAALASLLHVS.....TIGILMSAPNFVAVSKDFA 502

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 417779 seqs, 108206813 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2305

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	502	US-09-954-936-2	Sequence 2, Appli
2	401	79.9	502	US-09-892-985-8	Sequence 8, Appli
3	47	9.4	63	US-10-106-698-5644	Sequence 5644, Ap
4	45	9.0	70	US-09-899-495-87	Sequence 87, Appl
5	32	6.4	32	US-09-928-636A-25	Sequence 25, Appl
6	32	6.4	32	US-09-928-636A-27	Sequence 27, Appl
7	20	4.0	20	US-09-928-636A-6	Sequence 6, Appli
8	18	3.6	18	US-09-928-636A-5	Sequence 5, Appli
9	18	3.6	18	US-09-928-636A-8	Sequence 8, Appli
10	15	3.0	15	US-09-928-636A-4	Sequence 4, Appli
11	15	3.0	15	US-09-928-636A-18	Sequence 18, Appl
12	11	2.2	11	US-09-928-636A-7	Sequence 7, Appli
13	11	2.2	11	US-09-928-636A-9	Sequence 9, Appli
14	11	2.2	11	US-09-928-636A-19	Sequence 19, Appl
15	10	2.0	11	US-09-928-636A-10	Sequence 10, Appl
16	10	2.0	11	US-09-928-636A-17	Sequence 17, Appl
17	9	1.8	11	US-09-928-636A-3	Sequence 3, Appli
18	9	1.8	11	US-09-928-636A-11	Sequence 11, Appl
19	9	1.8	450	US-10-156-239-11	Sequence 11, Appl

20	9	1.8	450	9	US-10-199-485-11	Sequence 11, Appl
21	9	1.8	450	10	US-09-795-893-11	Sequence 11, Appl
22	8	1.6	11	9	US-09-928-636A-1	Sequence 1, Appli
23	8	1.6	11	9	US-09-928-636A-16	Sequence 16, Appl
24	8	1.6	245	9	US-09-895-913A-48	Sequence 48, Appl
25	8	1.6	431	10	US-09-835-270-4	Sequence 4, Appli
26	7	1.4	11	9	US-09-928-636A-2	Sequence 2, Appli
27	7	1.4	11	9	US-09-928-636A-12	Sequence 12, Appl
28	7	1.4	28	9	US-09-749-637A-301	Sequence 301, App
29	7	1.4	29	9	US-09-983-802-184	Sequence 184, App
30	7	1.4	37	9	US-09-983-802-399	Sequence 399, App
31	7	1.4	62	10	US-09-864-761-48905	Sequence 48905, A
32	7	1.4	70	9	US-09-749-637A-300	Sequence 300, App
33	7	1.4	73	9	US-10-051-643-141	Sequence 141, App
34	7	1.4	73	9	US-09-880-505-141	Sequence 141, App
35	7	1.4	79	10	US-09-881-752A-20	Sequence 20, Appl
36	7	1.4	84	9	US-10-050-704-134	Sequence 134, App
37	7	1.4	95	9	US-10-023-282-114	Sequence 314, App
38	7	1.4	157	9	US-10-046-938-4	Sequence 4, Appli
39	7	1.4	174	10	US-09-818-066-45	Sequence 45, Appl
40	7	1.4	174	10	US-09-818-066-48	Sequence 48, Appl
41	7	1.4	194	9	US-10-043-487-391	Sequence 391, App
42	7	1.4	213	9	US-10-043-487-374	Sequence 374, App
43	7	1.4	268	10	US-09-823-038A-14	Sequence 14, Appl
44	7	1.4	269	12	US-10-001-843-192	Sequence 192, App
45	7	1.4	289	9	US-10-043-487-299	Sequence 299, App

ALIGNMENTS

RESULT 1
US-09-954-936-2
; Sequence 2, Application US/09954936
; Publication No. US20030073161A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; FILE REFERENCE: 6017.US.01
; CURRENT APPLICATION NUMBER: US/09/954,936
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/771,737
; PRIOR FILING DATE: 1996-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: homo sapien
US-09-954-936-2

Query Match 100.0%; Score 502; DB 9; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGGVWLAALASLLHVSLLQSGFQRKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
Db 1 MRCSPGGVWLAALASLLHVSLLQSGFQRKLYKELVKNYNPLRPVANDSQPLTVVFSLL 60
QY 61 QIMDVDEKNQVLTINILQMSWTDHYLQWNVSEYGVKTVRPPDQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTINILQMSWTDHYLQWNVSEYGVKTVRPPDQIWKPDILLYNSADE 120
QY 121 RFDAETHNVLNNSGHCQVLPKGIKSSCYIDVWFPEVDVQHCCKLFGWSYGGWSJDL 180

Db 121 RFDAFHTNVLNNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGWSYGGWSLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPACOKH 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPACOKH 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 2

US-09-892-985-8
; Sequence 8, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-892-985-8
Query Match 79.9%; Score 401; DB 10; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGGVWALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQBLTVYFSLSL 60
Db 1 MRCSPGGVWALAAASLLHVSLSQGFQKLYKELVKNYNPLRPVANDSQBLTVYFSLSL 60
Qy 61 QIMDVDEKQVLTNINLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Db 61 QIMDVDEKQVLTNINLQMSWTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADE 120
Qy 121 RFDAFHTNVLNNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGWSYGGWSLDL 180
Db 121 RFDAFHTNVLNNSGHCQYLPGIFKSSCYIDVRWFFPDVQHCCLKFGWSYGGWSLDL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTWRRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAS 300
Qy 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPACOKH 360
Db 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPACOKH 360
Qy 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 3

US-10-106-698-5644
; Sequence 5644, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5644
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-106-698-5644

Query Match 9.4%; Score 47; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.8e-38;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 VCSEWFAACVDRCLCMASFVFTIICITIGILMSAPNFVEAVSKDFA 502
|||||
Db 17 VCSEWFAACVDRCLCMASFVFTIICITIGILMSAPNFVEAVSKDFA 63
|||||

RESULT 4

US-09-899-495-87
; Sequence 87, Application US/09899495
; Publication No. US20030088060A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Roberts, Steven L.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00188US1
; CURRENT APPLICATION NUMBER: US/09/899,495
; PRIORITY FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/215,815
; PRIORITY FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 60/216,481
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/216,479
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/216,482
; PRIORITY FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/217,096
; PRIORITY FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-495-87

Query Match 9.0%; Score 45; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.7e-36;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 SPTHDEHLHGQPPGPDPLAKILEEVRYIANRFRQDSEAVC 457
|||||
Db 1 SPTHDEHLHGQPPGPDPLAKILEEVRYIANRFRQDSEAVC 45
|||||

RESULT 5

US-09-928-636A-25
; Sequence 25, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B

; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-25

Query Match 6.4%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 NGEWDLVGIPGKRSERFYECCKEYPDVTFV 224
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Db 1 NGEWDLVGIPGKRSERFYECCKEYPDVTFV 32
|||||

RESULT 6

US-09-928-636A-27
; Sequence 27, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-928-636A-27

Query Match 6.4%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 1e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 SGVIPNGEWDLVGIPGKRSERFYECCKEYPD 219
|||||
Db 1 SGVIPNGEWDLVGIPGKRSERFYECCKEYPD 32
|||||

RESULT 7

US-09-928-636A-6
; Sequence 6, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13

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; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-6

Query Match          4.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 220
Db 1 IPGKRSERFYECCKEPYDV 20

RESULT 8
US-09-928-636A-5
; Sequence 5, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-5

Query Match          3.6%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 218
Db 1 IPGKRSERFYECCKEPYDV 18

RESULT 9
US-09-928-636A-8
; Sequence 8, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-8

Query Match          3.6%; Score 18; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 IPGKRSERFYECCKEPYDV 227
Db 1 YECCKEYPDVTFVTVMR 18

RESULT 10
US-09-928-636A-4
; Sequence 4, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-4

Query Match          3.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 GIPGKRSERFYECCCK 214
Db 1 GIPGKRSERFYECCCK 15

RESULT 11
US-09-928-636A-18
; Sequence 18, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-18
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Query Match 3.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 GIPGKRSERYECK 214
Db 1 GIPGKRSERYECK 15

RESULT 12
US-09-928-636A-7
; Sequence 7, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-7

Query Match 2.2%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 SERFYECKEP 216
Db 1 SERFYECKEP 11

RESULT 13
US-09-928-636A-9
; Sequence 9, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-9

Query Match 2.2%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 SERFYECKEP 216
Db 1 SERFYECKEP 11

RESULT 14
US-09-928-636A-19
; Sequence 19, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-19

Query Match 2.2%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 SERFYECKEP 216
Db 1 SERFYECKEP 11

RESULT 15
US-09-928-636A-10
; Sequence 10, Application US/09928636A
; Publication No. US20030092613A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Daniel H
; APPLICANT: Wang, Hoau-Yan
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Reitz, Allen B
; TITLE OF INVENTION: alpha7 nicotinic receptor peptides as ligands for beta
; FILE REFERENCE: beta amyloid peptides
; CURRENT APPLICATION NUMBER: US/09/928,636A
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-928-636A-10

Query Match 2.0%; Score 10; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 ERFYECKEP 216
Db 2 ERFYECKEP 11

Search completed: June 20, 2003, 19:23:18
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2003, 19:01:21 ; Search time 73 Seconds
(without alignments)
916.326 Million cell updates/sec

Title: US-09-954-936-2

Perfect score: 502

Sequence: 1 MRCSPGVWLAASLLHVS.....TIGILMSAPNFVAVSKDPA 502

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	502	19 AAW69216	V274T variant huma
2	401	79.9	502	15 AAW44153	Human neuronal nic
3	401	79.9	502	18 AAW09025	Neuronal nicotinic
4	401	79.9	502	21 AAB24088	Human PRO2145 prot
5	401	79.9	502	22 AAB82690	Nicotinic acetylch
6	401	79.9	502	22 AAB50012	Wild-type human al
7	300	59.8	502	22 AAB50015	Mutant human alpha
8	300	59.8	502	22 AAB50016	Mutant human alpha
9	229	45.6	502	22 AAB50017	Mutant human alpha
10	224	44.6	470	22 AAB50014	Chimeric alpha7/5-

11	202	40.2	448	22	AAW50018	Mature cell surfac
12	92	18.3	502	18	AAW12368	Neuronal alpha-bun
13	47	9.4	63	22	AAG74870	Human colon cancer
14	45	9.0	70	23	AAU83518	Beta amyloid ion ch
15	32	6.4	32	23	ABW76012	Beta amyloid bindi
16	32	6.4	32	23	ABW76014	Beta amyloid bindi
17	27	5.4	511	18	AAW12369	Neuronal alpha-bun
18	20	4.0	20	23	ABW5993	Beta amyloid bindi
19	18	3.6	18	23	ABW5992	Beta amyloid bindi
20	18	3.6	18	23	ABW5995	Beta amyloid bindi
21	15	3.0	15	23	ABW5991	Beta amyloid bindi
22	15	3.0	15	23	ABW5997	Beta amyloid bindi
23	13	2.6	21	22	AAE10084	Human ion channel
24	11	2.2	11	23	ABW5994	Beta amyloid bindi
25	11	2.2	11	23	ABW5996	Beta amyloid bindi
26	11	2.2	11	23	ABW76006	Beta amyloid bindi
27	10	2.0	11	23	ABW5997	Beta amyloid bindi
28	10	2.0	11	23	ABW76004	Beta amyloid bindi
29	10	2.0	250	22	ABG06105	Novel human diagno
30	10	2.0	279	22	AAU87310	Novel central nerv
31	10	2.0	304	22	ABG06104	Novel human diagno
32	10	2.0	304	22	ABG06107	Novel human diagno
33	10	2.0	457	22	AAW50013	Murine 5HT3 ligand
34	10	2.0	478	23	ABW88137	Human 5-Hydroxytry
35	10	2.0	478	23	AAU79383	Human 5-Hydroxytry
36	10	2.0	479	17	AAW89358	Alpha-9 nicotinic
37	9	1.8	11	23	ABW75990	Beta amyloid bindi
38	9	1.8	11	23	ABW75998	Beta amyloid bindi
39	9	1.8	85	22	AAE10085	Human ion channel
40	9	1.8	382	23	AAE21162	Human TRICH-6 prot
41	9	1.8	433	22	AAU00402	Mature human alpha
42	9	1.8	450	22	AAG67161	Amino acid sequenc
43	9	1.8	450	22	AAU00403	Human alpha nicoti
44	9	1.8	450	22	AAE00280	Human nicotinic ac
45	9	1.8	450	23	AAE21171	Human TRICH-15 pro

ALIGNMENTS

RESULT 1
AAW69216
ID AAW69216 standard; Protein; 502 AA.

XX AC AAW69216;

XX DT 09-OCT-1998 (first entry)

XX DE V274T variant human alpha7 nAChR protein.

XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease; schizophrenia.

XX OS Homo sapiens.

XX FN MO9828331-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23405.

XX PR 20-DEC-1996; 96US-0771737.

XX PA (ABBO) ABBOTT LAB.

XX PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

XX PI Roch J, Sullivan JF, Touma E;

XX DR WPI; 1998-377593/32.

XX DR N-PSDB; AAV44687.

XX

PT Nucleic acid encoding variant of human alpha7 nicotinic
PT acetylcholine receptor sub-unit - used to identify modulators of
PT the receptor, potentially useful for treating neuro-degeneration,
XX cancer, affective disorders etc.
PS Claim 15; Fig 2; 44pp; English.
XX
CC This sequence is the V247T variant of human alpha7 nicotinic
CC acetylcholine receptor (NACHR) subunit of the invention. Cells containing
CC the DNA are used to express the protein and to identify modulators of
CC alpha7 NACHR activity or cytoprotective agents, e.g. antisense
CC compounds or antagonists that are potentially useful for treating
CC neurodegeneration, enzyme dysfunction, affective disorders and immune
CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
CC psychosis and schizophrenia. Probes based on the DNA are used to detect
CC the DNA in usual hybridisation or amplification tests, while monoclonal
CC antibodies are used to detect the protein for diagnosis (in vitro or by
CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 NACHR,
CC the protein has about 100-fold greater sensitivity to cholinergic
CC receptor agonists (nicotine or acetylcholine) and response to these
CC agonists decays more slowly, but the wild-type inward rectification is
CC retained.
XX
SQ Sequence 502 AA;
Query Match 100.0%; Score 502; DB 19; Length 502;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRCSPGVWLAALASLLHVSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60
DB 1 MRCSPGVWLAALASLLHVSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60
QY 61 QIMDVEKQVLTNTIWLQMSWTDHYLQMVNVEYVGVKTVRFPDQIWKPDILLYNSADE 120
DB 61 QIMDVEKQVLTNTIWLQMSWTDHYLQMVNVEYVGVKTVRFPDQIWKPDILLYNSADE 120
QY 121 RDATFHTNVLNSSGHCQVLPGLFKSCYIDVRWFPFVQHCCLKFGSWSYGGWSLDL 180
DB 121 RDATFHTNVLNSSGHCQVLPGLFKSCYIDVRWFPFVQHCCLKFGSWSYGGWSLDL 180
QY 181 QMQEADISGYIPNGEWDLVGIPKGRSERFYECKPEYDPDVTFTVMRRRTLYGLNLLIP 240
DB 181 QMQEADISGYIPNGEWDLVGIPKGRSERFYECKPEYDPDVTFTVMRRRTLYGLNLLIP 240
QY 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
DB 241 CVLISALALLVFLPADSGEKISLGIITVLLSLTFFMLLVAEIMPATSDSVPLIAQYFAST 300
QY 301 MIIVGLSVVTVTVILOYHHDPDGGKMPKTRVILLNWCWFLMKRPGEDKVRPACQHK 360
DB 301 MIIVGLSVVTVTVILOYHHDPDGGKMPKTRVILLNWCWFLMKRPGEDKVRPACQHK 360
QY 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
DB 361 QRCCLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
QY 421 LHGGQPEGDPDLAKILEEYRYIANFRPCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
DB 421 LHGGQPEGDPDLAKILEEYRYIANFRPCODESEAVCSEWKFACVVDRLCLMAFSVFTI 480
QY 481 ICTIGILMSAPNFEAVSKDFA 502
DB 481 ICTIGILMSAPNFEAVSKDFA 502

RESULT 2
AAW44153
ID AAW44153 standard; Protein; 502 AA.
XX
AC AAW44153;
XX

DT 14-MAY-1998 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.
DE
XX Human neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
KW brain tissue; screening; NACHR; antibody.
XX
OS Homo sapiens.
XX
XX Location/Qualifiers
FH Key 1..23
FT Peptide /label= signal
FT 229..256
FT Domain /label= TMD1
FT /note= "transmembrane domain"
FT 262..284
FT Domain /label= TMD2
FT /note= "transmembrane domain"
FT 290..317
FT Domain /label= TMD3
FT /note= "transmembrane domain"
FT Misc-difference 343
FT /note= "encoded by CTS"
FT 462..487
FT Domain /label= TMD4
FT /note= "transmembrane domain"
FT 318..461
FT Domain /label= cytoplasmic_loop
XX
PN WO9420617-A2.
XX
XX 15-SEP-1994.
XX
XX 08-MAR-1994; 94WO-US02447.
XX
XX 08-MAR-1993; 93US-0028031.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Elliott KJ, Ellis SB, Harpold MM;
XX
XX WPI; 1994-303024/37.
XX N-PSDB; AAV12197.
XX
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
XX also transformed cells useful for screening cpds. which modulate
XX activity of the receptor
XX
XX Claim 7; Page 80-81; 99pp; English.
XX
XX The present sequence represents a human neuronal nicotinic acetylcholine
XX receptor (NACHR) subunit. The cells expressing the alpha and/or beta
XX NACHR subunits may be used in a method of screening compounds to
XX identify any which modulate the activity of human neuronal NACHR.
XX Subunit specific antibodies may be used to monitor the distribution
XX and expression density of various subunits in normal vs diseased brain
XX tissues. Testing of single receptor subunits or specific receptor
XX subunit combinations with a variety of potential agonists or antagonists
XX provides information with respect to the function and activity of the
XX individual subunits and should lead to the identification and design of
XX compounds that are capable of very specific interaction with one or
XX more receptor subtypes. The resulting drugs should exhibit fewer
XX unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
XX
SQ Sequence 502 AA;
Query Match 79.9%; Score 401; DB 15; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRCSPGVWLAALASLLHVSQGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSLSL 60

```
Db 1 MRCSPGVWLAALASLLHVSLSQGFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSLSLL 60
Qy 61 QIMDVDEKNQVLTNTNIWQSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNIWQSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLNNSGHCQVLPFGI FKSSCYIDVRWFFDVQHCCLKFGSWSGWSL 180
Db 121 RFDATFHTNVLNNSGHCQVLPFGI FKSSCYIDVRWFFDVQHCCLKFGSWSGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
```

RESULT 3

```
AAW09025
ID AAW09025 standard; Protein; 502 AA.
AC AAW09025;
XX
DT 09-APR-1997 (first entry)
DE Neuronal nicotinic acetylcholine receptor alpha-7 subunit.
KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW ligand-gated receptor.
XX
OS Homo sapiens.
XX
PN WO9641876-A1.
XX
PD 27-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US09775.
XX
PR 07-JUN-1995; 95US-0484722.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Harpold MW;
XX
DR WPI, 1997-065463/06.
DR N-PSDB; AAT48239.
XX
PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
used in screening to determine the effect of drugs on the receptor
XX
PS Disclosure; Page 73-74; 108pp; English.
XX
PN The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
CC acetylcholine receptor (nAChR) can be expressed in transfected
```

```
CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
CC cells, esp. mammalian cells or amphibian oocytes, expressing the
CC recombinant alpha-7 subunit, opt. in combination with other
CC recombinant alpha and/or beta subunits (see also AAW09018-24,
CC AAW09026-27), can be used to examine the function of human AChR and
CC to identify cpds. that modulate its activity.
XX
```

SQ Sequence 502 AA;

```
Query Match 79.9%; Score 401; DB 18; Length 502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRCSPGVWLAALASLLHVSLSQGFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSLSLL 60
Db 1 MRCSPGVWLAALASLLHVSLSQGFQRLKYLKELVKNYNPLRPVANDSQPLTVYFSLSLL 60
Qy 61 QIMDVDEKNQVLTNTNIWQSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Db 61 QIMDVDEKNQVLTNTNIWQSWTDHYLQMNVSSEYPGVKTVPDPGQIWKPDILLYNSADE 120
Qy 121 RFDATFHTNVLNNSGHCQVLPFGI FKSSCYIDVRWFFDVQHCCLKFGSWSGWSL 180
Db 121 RFDATFHTNVLNNSGHCQVLPFGI FKSSCYIDVRWFFDVQHCCLKFGSWSGWSL 180
Qy 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Db 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDVTFVTMRRTLYYGLNLLIP 240
Qy 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
Qy 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Db 301 MIIVGLSVVTVTVIQLYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
Qy 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
Qy 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Db 421 LHGGQPPGDPDLAKILEEVRYIANFRFCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
Qy 481 ICTIGILMSAPNFVEAVSKDFA 502
Db 481 ICTIGILMSAPNFVEAVSKDFA 502
```

RESULT 4

```
AAW09025
ID AAW09025 standard; Protein; 502 AA.
AC AAW09025;
XX
DT 29-JAN-2001 (first entry)
DE Human PRO2145 protein sequence SEQ ID NO:77.
XX
```

```
Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophage disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
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OS Homo sapiens.

```
XX
XX WO200053755-A2.
PN
XX
```

PD 14-SEP-2000.
 XX
 PF 06-JAN-2000; 2000WO-US00376.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58395.
 XX
 PS Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 PT
 XX Claim 61; Fig 58; 286pp; English.
 XX
 CC The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1037, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198, PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytic, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoele disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX
 XX Sequence 502 AA;
 SQ
 Query Match 79.9%; Score 401; DB 21; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRCSGGWALAAALSHVLSQGFQKLYKELVKNVNPVANDSQPLTVFSL 60
 DB 1 MRCSGGWALAAALSHVLSQGFQKLYKELVKNVNPVANDSQPLTVFSL 60
 QY 61 QIMDVDEKQVLTNTLWQSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTLWQSWTDHYLQWNVSEYPGVKTVPDQIWKPDILLYNSADE 120
 QY 121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCXKLFSGWSYGSWLDL 180
 DB 121 RFDATHTNVLNNSGHCQYLPFGIFKSSCYIDVRWPFDFVQHCXKLFSGWSYGSWLDL 180
 QY 181 QMQEADISGYPNGEWDLVGIPGKRSRFEYECCKEYPDVFTVTMRRTLYGLNLLIP 240
 DB 181 QMQEADISGYPNGEWDLVGIPGKRSRFEYECCKEYPDVFTVTMRRTLYGLNLLIP 240
 QY 241 CVLISALALVFLPADSGEKISLGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300

Db 241 CVLISALALVFLPADSGEKISLGITVLLSLTFVFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLOVHHDDPDGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 Db 301 MIIVGLSVVTVIVLOVHHDDPDGKMPKWTTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDGSGVCGRMACSPTHDEHL 420
 QY 421 LHGQPPGEGDPLAKILEEVRYIANRPRCODESAVCSWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGQPPGEGDPLAKILEEVRYIANRPRCODESAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502
 RESULT 5
 AAB82690
 ID AAB82690 standard; Protein; 502 AA.
 XX
 AC AAB82690;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Nicotinic acetylcholine receptor alpha7.
 XX
 KW Nicotinic acetylcholine receptor; nAChR; human;
 KW acetylcholine binding protein; AChBP; mollusc;
 KW ligand-binding protein; ligand-gated ion channel; crystal;
 KW drug design; protein co-ordinate data; schizophrenia;
 KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
 KW therapy; nootropic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 108..115
 FT /note= "conserved ligand-binding region, residues
 FT Tpr108 and Tpr115 are essential"
 FT Region 171..173
 FT /note= "conserved ligand-binding region, residues
 FT Tpr171 and Tpr173 are essential"
 FT Region 210..217
 FT /note= "conserved ligand-binding region, residues
 FT Tyr210, Cys212, Cys213 and Tyr217 are
 FT essential"
 XX
 FN WO200158951-A2.
 XX
 PD 16-AUG-2001.
 XX
 DP 09-FEB-2001; 2001WO-EP01457.
 XX
 PR 10-FEB-2000; 2000EP-0200443.
 PR 31-OCT-2000; 2000EP-0203810.
 XX
 PA (TEWE-) STICHTING TECH WETENSCHAPPEN.
 XX
 PI Smit AB, Sixma TK;
 XX
 DR WPI; 2001-497071/54.
 XX
 PT Water-soluble ligand-binding proteins derived from molluscs and analogues
 PT of ligand-gated ion channels, useful in drug screening assay, where the
 PT drugs identified can be used in the treatment of Alzheimer's disease or
 PT schizophrenia -
 PS Disclosure; Page 252-254; 260pp; English.

CC The present sequence is that of the alpha subunit of human
 CC nicotinic acetylcholine receptor (nAChR). The sequence includes
 CC regions that are conserved throughout the various nAChR alpha
 CC subunits and which are essential for ligand binding. The invention
 CC relates to water-soluble ligand-binding proteins derived from
 CC molluscs, especially acetylcholine-binding proteins (AChBPs) and
 CC analogues of ligand-gated ion channels, their crystals, and their
 CC use for screening ligands of ligand-gated ion channels. The
 CC water-soluble ligand-binding proteins are capable of forming
 CC multimers and are amenable to crystallization. The crystal
 CC structure of AChBP is provided, and can be used to generate 3D
 CC models of the extracellular ligand-binding domain of ligand-gated
 CC ion channels and thus for screening of drugs that act on these
 CC ion channels. Chimeric proteins are provided that are capable of
 CC binding a ligand of a ligand-gated receptor, and comprise at
 CC least the amino acids of the AChBP determining solubility of the
 CC AChBP, in the same positions as in the AChBP, and also comprising
 CC amino acids determining binding to the ligand. In the chimeric
 CC proteins, at least the essential amino acids of at least 1 of the
 CC conserved regions of an nAChR have been substituted for the
 CC corresponding amino acids, and preferably entire stretches have
 CC been substituted. New drugs can be developed that selectively
 CC intervene in neuronal signalling pathways, especially where the
 CC ligand-gated ion channel is the nAChR, and the related disorder is
 CC Tourette's syndrome, Alzheimer's disease, addiction to nicotine
 CC or schizophrenia.
 CC
 XX
 SQ Sequence 502 AA;

Query Match 79.9%; Score 401; DB 22; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
 QY 121 RPDATFTNNVLSNGSHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
 DB 121 RPDATFTNNVLSNGSHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGRSRERFYECCKEYPDYTFVTMMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGRSRERFYECCKEYPDYTFVTMMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPEGDPDLAKILEEVRYITANFRCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGQPEGDPDLAKILEEVRYITANFRCODESEAVCSWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 6
 AAB50012
 ID AAB50012 standard; Protein; 502 AA.

XX AAB50012;
 AC 14-WAR-2001 (first entry)
 DT Wild-type human alpha7 ligand gated ion channel.
 DE Human; alpha7 nicotinic acetylcholine gated ion channel;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance.
 XX Homo sapiens.
 OS WO2000073431-A2.
 PN 07-DEC-2000.
 PD 25-MAY-2000; 2000WO-US11862.
 XX 27-MAY-1999; 99US-0136174.
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 DR N-PSDB; AAC90380.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 XX
 PS Disclosure; Pages 61-63; 77pp; English.
 CC The present sequence is wild-type human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.

SQ Sequence 502 AA;

Query Match 79.9%; Score 401; DB 22; Length 502;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGGVWLAALASLLHVSLLQGEFQRLKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
 DB 61 QIMDVEKNQVLTNNIWLQMSWTDHYLQMNVSYPGVKTRFPDQGIWKPDILLYNSADE 120
 QY 121 RPDATFTNNVLSNGSHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
 DB 121 RPDATFTNNVLSNGSHCQYLPFGIFKSSCYIDVRWPFDFVQHCKLFGSGWSYGGSLDL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGRSRERFYECCKEYPDYTFVTMMRRRTLYYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGRSRERFYECCKEYPDYTFVTMMRRRTLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 CVLISALALLVFLPADSGEKISLGITVLLSLTTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 DB 301 MIIVGLSVVTVIVLQYHHDDPGGKMPKTRVILLNWCWFLRMKRPGEKVRPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420

Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGPDPLAKILEEVRYIANFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGPDPLAKILEEVRYIANFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 7
 AAB50015
 ID AAB50015 standard; Protein; 502 AA.
 AC AAB50015;
 XX
 DT 14-MAR-2001 (first entry)
 DE Mutant human alpha7 ligand gated ion channel #1.
 KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 230
 FT /note= "Wild-type Thr substituted by Pro"
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR N-PSDB; AAC90385.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 XX Claim 100; Pages 70-72; 77pp; English.

XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.
 XX
 XX Sequence 502 AA;
 SQ

Query Match 59.8%; Score 300; DB 22; Length 502;
 Best Local Similarity 99.6%; Pred. No. 2.8e-282;
 Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLSQGFQRLKYKELVKNYNPLRPVANDSQPLTVVFSLL 60
 Db 1 MRCSPGVWLAALASLLHVSLSQGFQRLKYKELVKNYNPLRPVANDSQPLTVVFSLL 60
 QY 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120

Db 61 QIMDVDEKNQVLTNIWLQMSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
 QY 121 RFDATFTNVLNVSCHCQYLPGI PKSSCVIDVRWPFDDVQHCKLFGSWSYGGWSL 180
 Db 121 RFDATFTNVLNVSCHCQYLPGI PKSSCVIDVRWPFDDVQHCKLFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPEYPDVTFTVTMRRRLYYGLNLLIP 240
 Db 181 QMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPEYPDVTFTVTMRRRLYYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 Db 241 CVLISALALLVFLPADSGEKISLGITVLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVPACQHK 360
 Db 301 MIIVGLSVVTVIVLQVHHDDPGGKMPKTRVILLNWCWFLRMKPGEDKVPACQHK 360
 QY 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 Db 361 QRRCSLASVEMSAVAPPPASNGNLLYIGFRGLDGVHCVPTPDSGVVCGRMACSPTHDEHL 420
 QY 421 LHGGQPPGPDPLAKILEEVRYIANFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 Db 421 LHGGQPPGPDPLAKILEEVRYIANFRQCODESEAVCSEWKFAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 Db 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 8
 AAB50016
 ID AAB50016 standard; Protein; 502 AA.
 XX
 AC AAB50016;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Mutant human alpha7 ligand gated ion channel #2.
 KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 241
 FT /note= "Wild-type Cys substituted by Ser"
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA
 PI Groppi VE, Wolfe ML, Berkenpas MB;
 XX
 DR WPI; 2001-061524/07.
 DR N-PSDB; AAC90386.
 XX
 PT Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 XX Claim 102; Pages 72-74; 77pp; English.

XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.

XX Sequence 502 AA;

Query Match 59.8%; Score 300; DB 22; Length 502;
 Best Local Similarity 99.6%; Pred. No. 2.8e-282;
 Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQRLKYLKVNINPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGVWLAALASLLHVSLOGEFQRLKYLKVNINPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
 QY 121 RFDATEFTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 RFDATEFTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRLTYGLNLLIP 240
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRLTYGLNLLIP 240
 QY 241 CVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 DB 241 SVLISALALLVFLPADSGEKISLGITVLLSLTFMLLVAEIMPATSDSVPLIAQYFAST 300
 QY 301 MIIVGLSVVTVTVLQYHHHDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPAQCHK 360
 DB 301 MIIVGLSVVTVTVLQYHHHDPGGKMPKTRVILLNWCWFLRMKRPGEKDKVRPAQCHK 360
 QY 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDGSGVWCGRMACSPTHDEHL 420
 DB 361 QRRCSLASVEMSAVAPPASNGNLLYIGFRGLDGVCVPTPDGSGVWCGRMACSPTHDEHL 420
 QY 421 LHGGOPPEGDPLAKILEEVRYIANFRFCODESEAVCSEWKAACVVDRLCLMAFSVFTI 480
 DB 421 LHGGOPPEGDPLAKILEEVRYIANFRFCODESEAVCSEWKAACVVDRLCLMAFSVFTI 480
 QY 481 ICTIGILMSAPNFVEAVSKDFA 502
 DB 481 ICTIGILMSAPNFVEAVSKDFA 502

RESULT 9
 AAB50017
 ID AAB50017 standard; Protein; 502 AA.

XX AAB50017;

DT 14-MAR-2001 (first entry)

DE Mutant human alpha7 ligand gated ion channel #3.

KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; tutein.

XX Homo sapiens.

OS Synthetic.

TH Key Location/Qualifiers

FT Misc-difference 230

FT /note= "Wild-type Thr substituted by Pro"

FT Misc-difference 241

FT /note= "Wild-type Cys substituted by Ser"

XX WO200073431-A2.
 XX 07-DEC-2000.
 XX 25-MAY-2000; 2000WO-US11862.
 XX 27-MAY-1999; 99US-0136174.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX N-PSDB; AAC90387.
 XX Special cell culture medium for treating cells and for inducing
 XX mammalian cell lines to conduct calcium ions, comprising specified
 XX concentrations of ions of sodium, calcium and potassium at specified pH
 XX Claim 104; Pages 75-77; 77pp; English.
 XX The present sequence is a mutant human alpha7 nicotinic acetylcholine
 CC gated ion channel. The human alpha7 ion channel was used in the
 CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
 CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
 CC ion channel can be expressed by recombinant cells in the present
 CC invention, resulting in preferential calcium ion conductance by the
 CC cells.

XX Sequence 502 AA;

Query Match 45.6%; Score 229; DB 22; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2.2e-213;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRCSPGVWLAALASLLHVSLOGEFQRLKYLKVNINPLRPVANDSQPLTVYFSL 60
 DB 1 MRCSPGVWLAALASLLHVSLOGEFQRLKYLKVNINPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
 DB 61 QIMDVDEKQVLTNTNIWLQSWTDHYLQWNVSEYPGVKTVPDPGQIWKPDILLYNSADE 120
 QY 121 RFDATEFTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 DB 121 RFDATEFTNVLNNSGHCQYLPPGIFKSSCYIDVRWPFDFVQHCKLKFGSWSYGGWSL 180
 QY 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRLTYGLNLLIP 229
 DB 181 QMQEADISGYIPNGEWDLVGIPGKRSEFYECCKEYPDPVTFVTMRRRLTYGLNLLIP 229

RESULT 10

AAB50014

ID AAB50014 standard; Protein; 470 AA.

XX AAB50014;

DT 14-MAR-2001 (first entry)

DE Chimeric alpha7/5-HT3 ligand gated ion channel.

KW Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.

XX Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX WO200073431-A2.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US11862.
 XX 27-MAY-1999; 99US-0136174.
 XX (PHAA) PHARMACIA & URJOHN CO.
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX N-PSDB; AAC90382.
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT .
 XX Claim 97; Pages 66-68; 77pp; English.
 XX The present sequence is a chimeric human alpha7 nicotinic
 CC acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand gated ion
 CC channel. The alpha7/5-HT3 chimeric ion channel can be expressed by
 CC recombinant cells in the present invention, resulting in preferential
 CC calcium ion conductance by the cells.
 XX Sequence 470 AA;
 SQ
 Query Match 44.6%; Score 224; DB 22; Length 470;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-208;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 Db 1 MRCSPGGWALAAASLLHVSLOGEFQKLYKELVKNYNPLRPVANDSQPLTVYFSL 60
 QY 61 QIMDVDEKQVLTNNIWLQSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
 Db 61 QIMDVDEKQVLTNNIWLQSWTDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADE 120
 QY 121 RFDATFTNNVNSSGHCOYLPDGIKSSCYIDVRWPFDDVQHCKLFGSGWSYGGWSL 180
 Db 121 RFDATFTNNVNSSGHCOYLPDGIKSSCYIDVRWPFDDVQHCKLFGSGWSYGGWSL 180
 QY 181 QMOEADISGYPNGEWDLVGIPGRSERFYECCKEPYPDVTFV 224
 Db 181 QMOEADISGYPNGEWDLVGIPGRSERFYECCKEPYPDVTFV 224
 RESULT 11
 AAB50018
 ID AAB50018 standard; Protein; 448 AA.
 XX AAB50018;
 XX AC
 XX 14-MAR-2001 (first entry)
 XX DE Mature cell surface chimeric alpha7/5-HT3 ligand gated ion channel.
 XX Murine; alpha7 nicotinic acetylcholine gated ion channel; human;
 XX 5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutant.
 XX Chimeric - Mus musculus.
 XX Chimeric - Homo sapiens.
 XX WO2000073431-A2.
 XX PN
 XX 07-DEC-2000.
 XX PD
 XX 25-MAY-2000; 2000WO-US11862.
 XX PF
 XX 27-MAY-1999; 99US-0136174.
 XX PR
 XX (PHAA) PHARMACIA & URJOHN CO.

XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI; 2001-061524/07.
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT .
 XX Disclosure; Fig 2; 77pp; English.
 XX The present sequence is the mature cell surface form of a chimeric human
 CC alpha7 nicotinic acetylcholine/murine 5-hydroxytryptamine (5-HT3) ligand
 CC gated ion channel (the full protein sequence is given in AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells.
 XX Sequence 448 AA;
 SQ
 Query Match 40.2%; Score 202; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. NO. 3.2e-187;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 GEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLLOIMDVDEKQVLTNNIWLQSW 82
 Db 1 GEFORKLYKELVKNYNPLRPVANDSQPLTVYFSLSLLOIMDVDEKQVLTNNIWLQSW 60
 QY 83 TDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADERFDATFTNNVNSSGHCOYLP 142
 Db 61 TDHYLQMNVSYPGVKTVRFPDQIWKPDILLYNSADERFDATFTNNVNSSGHCOYLP 120
 QY 143 PGIFKSSCYIDVRWPFDDVQHCKLFGSGWSYGGWSLQMOEADISGYPNGEWDLVGIP 202
 Db 121 PGIFKSSCYIDVRWPFDDVQHCKLFGSGWSYGGWSLQMOEADISGYPNGEWDLVGIP 180
 QY 203 GKRSERFYECCKEPYPDVTFV 224
 Db 181 GKRSERFYECCKEPYPDVTFV 202
 RESULT 12
 AAW12368
 ID AAW12368 standard; Protein; 502 AA.
 XX AAW12368;
 XX AC
 XX 17-JUN-1997 (first entry)
 XX DT
 XX DE Neuronal alpha-bungarotoxin binding protein alpha subunit.
 XX DE Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
 XX KW ligand binding; ion channel.
 XX OS Gallus sp.
 XX Key Location/Qualifiers
 FT Peptide 1..22 /label= Sig_peptide
 FT Protein 23..502 /label= Mat_protein
 FT US5599709-A.
 XX PN
 XX 04-FEB-1997.
 XX PD
 XX 28-SEP-1989; 89US-0413947.
 XX PF
 XX 28-SEP-1989; 89US-0413947.
 XX PR
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX PA

PI Lindstrom JM, Schoepfer RD;
 XX WPI; 1997-118297/11.
 DR N-PSDB; AAT59196.
 XX
 PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
 PT to screen cholinergic agents and other drugs which may affect ligand
 PT binding, ion channel or other activities of the protein.
 XX
 PS Example; Fig 2A-B; 18pp; English.
 XX
 CC The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
 CC sequences of chick neuronal alpha-bungarotoxin binding protein
 CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
 CC obt'd. from an 18-day chick embryo cDNA library. ABBP subunits can
 CC be produced in recombinant host cells, pref. a bacterium, and used
 CC in the screening of cholinergic agents and other drugs that may
 CC affect the ligand binding, ion channel or other activity of intact
 CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.
 XX
 SQ Sequence 502 AA;
 Query Match 18.3%; Score 92; DB 18; Length 502;
 Best Local Similarity 100.0%; Pred. No. 2e-80;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 275 FMLLVAEIMPATSDSVPLIAQYFASTMIIIVGLSVVTVIVLYHHDDPGGKMPKTRVI 334
 DB 275 FMLLVAEIMPATSDSVPLIAQYFASTMIIIVGLSVVTVIVLYHHDDPGGKMPKTRVI 334
 QY 335 LLNCAWFLMRKRPGEKVRPACQHKQRCSL 366
 DB 335 LLNCAWFLMRKRPGEKVRPACQHKQRCSL 366
 RESULT 13
 ID AAG74870 standard; Protein; 63 AA.
 XX
 AC AAG74870;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:5634.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 15.
 XX
 OS Homo sapiens.
 XX
 FN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI; 2001-235357/24.
 DR N-PSDB; AAH34275.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11; Page 7187; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing P.
 CC Additionally, N may be used to supplement the patients own production of P,
 CC by inserting the nucleic acids into a host cell and culturing the cell,
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 63 AA;
 Query Match 9.4%; Score 47; DB 22; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.6e-37;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 456 VCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFVEAVSKDFA 502
 DB 17 VCSWKFAACVVDRLCLMAFSVFTIICITIGILMSAPNFVEAVSKDFA 63
 RESULT 14
 AAU83518
 ID AAU83518 standard; Protein; 70 AA.
 XX
 AC AAU83518;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Novel human ion channel ion-118.
 XX
 KW Ion channel; brain; mental disorder; human immunodeficiency virus;
 KW HIV; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;
 KW inflammatory condition; Crohn's disease; rheumatoid arthritis;
 KW autoimmune disorder; movement disorder; CNS disorder; pain;
 KW neuropathic pain; migraine; headache; stroke; psychotic disorder;
 KW neurological disorder; anxiety; schizophrenia; dementia; dyskinesia;
 KW Huntington's disease; Tourette's syndrome; degenerative disorder;
 KW Parkinson's disease; Alzheimer's disease; ataxia; metabolic disorder;
 KW cardiovascular disease; diabetes; obesity; anorexia; hypotension;
 KW hypertension; thrombosis; atherosclerosis; proliferative disease;
 KW cancer; hyperproliferative disorder; psoriasis.
 XX
 OS Homo sapiens.
 XX
 FN WO200202639-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-US21287.
 XX
 PR 05-JUL-2000; 2000US-215815P.
 PR 06-JUL-2000; 2000US-216479P.
 PR 06-JUL-2000; 2000US-216481P.
 PR 06-JUL-2000; 2000US-216482P.
 PR 10-JUL-2000; 2000US-217096P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Benjamin CW, Roberts SL, Karnovsky AM, Ruble CL;
 XX
 DR WPI; 2002-140086/18.

DR N-PSDB; ABK33299.
 XX Novel polynucleotide and polypeptides of human ion channels for
 PT screening modulators useful for treating and diagnosing diseases e.g.
 PT obesity, anorexia, anxiety, schizophrenia, dementia
 XX
 XX Claim 2; Page 94; 193pp; English.
 PS
 CC The invention describes an isolated polynucleotide (I) comprising a
 CC sequence encoding a polypeptide ion channel. The polypeptide (II) is
 CC useful for inducing an immune response in a mammal against (II); and for
 CC identifying a modulator of (II) activity. (I)/(II) are useful for
 CC screening a human subject to diagnose a disorder affecting the brain
 CC especially ion-channel related mental disorder genotype or its genetic
 CC predisposition or identifying an ion channel allelic variant that
 CC correlates with mental disorder, where a biological sample comprising
 CC nucleic acid from human patient diagnosed with mental disorders or from
 CC patients genetic progenitors or progeny is provided. Examples of the
 CC disorders include disease and conditions as infections, such as viral
 CC infections caused by human immunodeficiency virus (HIV); thyroid
 CC disorders (e.g. thyrotoxicosis, myxoedema); renal failure; inflammatory
 CC conditions (e.g. Crohn's disease); rheumatoid arthritis; autoimmune
 CC disorders; CNS disorders (e.g. pain including neuropathic pain, migraine,
 CC and other headaches); stroke; psychotic and neurological disorders
 CC including anxiety, schizophrenia, dementia; dyskinesias, such as
 CC Huntington's disease or Tourette's syndrome; degenerative disorders such
 CC as Parkinson's, Alzheimer's; movement disorders, including ataxias;
 CC metabolic and cardiovascular disease and disorders e.g. diabetes;
 CC obesity, anorexia, hypotension, hypertension, thrombosis, and
 CC atherosclerosis, proliferative disease and cancer and hyperproliferative
 CC disorders such as psoriasis. This is the amino acid sequence of a novel
 CC ion channel, described in the method of the invention.
 XX
 SQ Sequence 70 AA;
 Query Match 9.0%; Score 45; DB 23; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.5e-35;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 413 SPTHDHLHGQPPGPDPLAKILBEVRYIANFRQDSEAVC 457
 Db 1 SPTHDHLHGQPPGPDPLAKILBEVRYIANFRQDSEAVC 45
 RESULT 15
 ID ABB76012 standard; Peptide; 32 AA.
 AC ABB76012;
 XX
 DT 12-JUL-2002 (first entry)
 DE Beta amyloid binding peptide huma7.
 XX
 KW Beta amyloid; alpha 7 nicotinic acetylcholine receptor; nAChR;
 KW receptor; human; Alzheimer's disease; antiparkinsonian;
 KW analgesic; antidepressant; tranquilizer; neuroleptic; diagnosis;
 KW therapy; drug screening.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Misc-difference 1..32 /note= "the peptide preferably contains at least
 FT one D-form residue"
 FT Modified-site 32 /note= "C-terminal amide"
 FT
 XX WO200214351-A2.
 PN
 XX
 PD 21-FEB-2002.

XX
 PF 14-AUG-2001; 2001WO-US25410.
 XX
 PR 14-AUG-2000; 2000US-225048P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 XX Lee DHS, Reitz AB, Plata-Salaman C, Wang H;
 PI
 XX WPI; 2002-371643/40.
 DR
 XX New beta amyloid binding peptides, useful in the diagnosis of
 PT Alzheimer's disease, Parkinson's disease or pain and in development of
 PT high throughput screening, or computer-based rationale drug design to
 PT create small molecule mimetics -
 XX
 XX Claim 1; Page 36; 39pp; English.
 PS
 XX The present sequence is that of beta amyloid binding peptide
 CC huma7 derived from the human alpha 7 nicotinic acetylcholine
 CC receptor (nAChR). The peptide, which is preferably N-acetylated
 CC and C-amidated, can be synthetically produced using D or L isomeric
 CC amino acid precursors. It is one of a set of claimed beta amyloid
 CC binding peptides (see ABB75988-ABB76015). These peptides can be
 CC used in a method for diagnosing Alzheimer's disease (AD) by binding
 CC to beta amyloid. This enables the measurement of free beta
 CC amyloid(1-40) or beta amyloid(1-42) present in biological tissues
 CC or fluids in AD patients, or those in the early stages of AD, or who
 CC will develop AD in the future. The binding reaction of these
 CC peptides and beta amyloid can also be used in drug screening assays
 CC to identify small molecule modulators of alpha 7 nAChR for treating
 CC neurodegenerative disorders such as AD, Parkinson's disease, pain,
 CC neuropathic pain, depression, anxiety, obsessive compulsive
 CC behaviour, phobia, post-traumatic stress, panic, schizophrenia,
 CC psychosis, bipolar disorder, dementia and substance abuse. The
 CC claimed peptides can also be therapeutically active agents, or
 CC can be used to model interactions with beta amyloid for rational
 CC drug design. Hum7 peptide attenuated beta amyloid's inhibition
 CC of potassium-evoked acetylcholine release from rodent synaptosomes
 CC (IC50 = 0.362 uM). Acetylcholine release inhibition at 100 uM was
 CC 90%. Huma7 peptide also inhibited 125I-beta amyloid binding to
 CC alpha 7 SK-N-MC membranes and beta amyloid(1-32) deposition onto
 CC synthaloid plates.
 XX
 SQ Sequence 32 AA;
 Query Match 6.4%; Score 32; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.2e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 193 NGEWDLVGIPGKRSERFYECCKEPYDVTFTV 224
 Db 1 NGEWDLVGIPGKRSERFYECCKEPYDVTFTV 32
 Search completed: June 20, 2003, 19:11:37
 Job time : 75 secs